

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala  
 50 55 60  
 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala  
 65 70 75 80  
 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile  
 85 90 95  
 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr  
 100 105 110  
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala  
 115 120 125  
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu  
 130 135 140  
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala  
 145 150 155 160  
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu  
 165 170 175  
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val  
 180 185 190  
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala  
 195 200 205  
 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr  
 210 215 220  
 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu  
 225 230 235 240  
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro  
 245 250 255  
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu  
 260 265 270  
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr  
 275 280 285  
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr  
 290 295 300  
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser  
 305 310 315 320  
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn  
 325 330 335  
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp  
 340 345 350  
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile  
 355 360 365  
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe

370					375					380					
Ser 385	Pro	Arg	Gly	Val	Ala 390	Gly	Ile	Asp	Gly	Ser 395	Val	Ala	Gln	Ala	Ile 400
Gly	Thr	Ser	Leu	Ala 405	Val	Gln	Ser	Arg	His 410	Pro	Asp	Glu	Ile	Arg	Ala 415
Pro	Arg	Thr	Val 420	Ala	Leu	Leu	Gly	Asp 425	Leu	Ser	Phe	Leu	His	Asp	Ile 430
Gly	Gly	Leu 435	Leu	Ile	Gly	Pro	Asp 440	Glu	Pro	Arg	Pro	Glu 445	Asn	Leu	Thr
Ile 450	Val	Val	Ser	Asn	Asp 455	Asn	Gly	Gly	Gly	Ile	Phe 460	Glu	Leu	Leu	Glu
Thr 465	Gly	Ala	Asp	Gly 470	Leu	Arg	Pro	Asn	Phe	Glu 475	Arg	Ala	Phe	Gly	Thr 480
Pro	His	Asp	Ala	Ser 485	Ile	Ala	Asp	Leu	Cys 490	Ala	Gly	Tyr	Gly	Ile 495	Glu
His	Gln	Val	Val 500	Asp	Asn	Leu	Gln	Asp 505	Leu	Ile	Ile	Ala	Leu	Val	Asp 510
Thr	Thr	Glu 515	Val	Ser	Gly	Phe	Thr 520	Ile	Ile	Glu	Ala	Ser 525	Thr	Val	Arg
Asp 530	Thr	Arg	Arg	Ala	Gln 535	Gln	Gln	Ala	Leu	Met	Asp 540	Thr	Val	His	

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<210> 875
<211> 1080
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1057)
<223> RXA02319
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<400> 875
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agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115
Met Ser Asn Tyr Ser
1 5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
10 15 20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
25 30 35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn
40 45 50

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gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac 307  
 Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His  
 55 60 65

gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc 355  
 Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly  
 70 75 80 85

ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa 403  
 Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln  
 90 95 100

cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc 451  
 Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg  
 105 110 115

gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa 499  
 Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys  
 120 125 130

gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc 547  
 Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg  
 135 140 145

acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc 595  
 Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly  
 150 155 160 165

ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc 643  
 Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg  
 170 175 180

caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac 691  
 Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp  
 185 190 195

gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac 739  
 Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn  
 200 205 210

gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg 787  
 Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met  
 215 220 225

caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa 835  
 Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu  
 230 235 240 245

aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc 883  
 Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr  
 250 255 260

ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc 931  
 Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu  
 265 270 275

atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg 979  
 Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met  
 280 285 290

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa  
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct  
1077

Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
310 315

aaa  
1080

<210> 876

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 876

Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala  
1 5 10 15

Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His  
20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg  
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met  
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr  
210 215 220



Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp  
225 230 235 240

His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn  
245 250 255

Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu  
260 265 270

Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr  
275 280 285

Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe  
290 295 300

Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
305 310 315

<210> 877

<211> 1017

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(994)

<223> RXS00393

<400> 877

tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60

aattgcgcga tcgagtatgt gatggggaaa gatagagggt atg tct cac acg gaa 115  
Met Ser His Thr Glu  
1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly  
25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259  
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307  
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp  
55 60 65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355  
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu  
70 75 80 85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403  
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala  
90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451  
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser  
                   105                                  110                                  115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499  
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu  
                   120                                  125                                  130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547  
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly  
                   135                                  140                                  145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595  
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met  
                   150                                  155                                  160                                  165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643  
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala  
                                   170                                  175                                  180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691  
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn  
                                   185                                  190                                  195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu  
                   200                                  205                                  210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
                   215                                  220                                  225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
                   230                                  235                                  240                                  245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883  
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala  
                                   250                                  255                                  260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc 931  
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile  
                                   265                                  270                                  275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg 979  
 Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu  
                   280                                  285                                  290

gca tta gcg ttt agc taaaacgctt ttgcagctc ccc  
 1017  
 Ala Leu Ala Phe Ser  
                   295

&lt;210&gt; 878

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 878

Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp

1	5	10	15
Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val	20	25	30
Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala	275	280	285
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser	290	295	

&lt;210&gt; 879

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(982)

&lt;223&gt; FRXA00393

&lt;400&gt; 879

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tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60

aattgcgcgga tcgagtatgt gatgggggaaa gatagagggtt atg tct cac acg gaa 115
                                         Met Ser His Thr Glu
                                         1           5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
              10              15              20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
              25              30              35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
              40              45              50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
              55              60              65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
              70              75              80              85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
              90              95              100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
              105              110              115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
              120              125              130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
              135              140              145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
              150              155              160              165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
              170              175              180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
              185              190              195

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aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu  
200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883  
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala  
250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931  
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser  
265 270 275

gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979  
Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp  
280 285 290

cat tagcgtttag ctaaaacgct ttt  
1005  
His

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<210> 880
<211> 294
<212> PRT
<213> Corynebacterium glutamicum
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<400> 880  
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Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val  
20 25 30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp  
35 40 45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
50 55 60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
65 70 75 80

Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
85 90 95

Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
100 105 110

Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
115 120 125

Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro

130											135											140
Tyr 145	Gly	Tyr	Arg	Gly	Leu 150	Gly	Glu	Ile	Ala	Val 155	Phe	Ile	Phe	Phe	Gly 160							
Leu	Val	Ala	Val	Met 165	Gly	Thr	Gln	Phe	Thr 170	Gln	Thr	Gly	Ser	Val 175	Ser							
Trp	Ala	Gly	Leu 180	Ala	Ala	Ala	Val	Gly 185	Val	Gly	Ser	Met	Ser 190	Ala	Gly							
Val	Asn 195	Leu	Ala	Asn	Asn	Ile	Arg 200	Asp	Ile	Pro	Thr	Asp 205	Ser	Lys	Thr							
Gly 210	Lys	Ile	Thr	Leu	Ala	Val 215	Arg	Leu	Gly	Asp	Ala 220	Gly	Ala	Arg	Lys							
Leu 225	Phe	Leu	Ala	Leu	Ile 230	Ser	Thr	Pro	Phe	Ile 235	Met	Ser	Ile	Cys	Leu 240							
Ala	Phe	Val	Ala	Trp 245	Pro	Ala	Leu	Ile	Ala 250	Ile	Ile	Val	Phe	Pro 255	Leu							
Ala	Leu	Lys	Ala 260	Ala	Gly	Pro	Ile	Arg 265	Asn	Asn	Ala	Thr	Gly 270	Lys	Asp							
Leu	Ile 275	Pro	Ser	Ser	Ala	Gln	Gln 280	Gly	Ala	Pro	Trp	Arg 285	Cys	Gly	Pro							
Cys 290	Ser	Arg	Ala	Trp	His																	

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<210> 881
<211> 843
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(820)  
<223> RXA00391
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<400> 881
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tttctcccc atccctgtac aagataaaac cctgtcacag ttg ctg cgc gat tct 115
                                         Leu Leu Arg Asp Ser
                                         1                     5

caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc 163
Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala
                        10                      15                      20

act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg 211
Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu
                        25                      30                      35

aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa 259
Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu
                        40                      45                      50

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ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307  
 Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln  
 55 60 65

gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355  
 Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp  
 70 75 80 85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403  
 Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu  
 90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451  
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln  
 105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499  
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu  
 120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547  
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg  
 135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595  
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser  
 150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643  
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly  
 170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691  
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met  
 185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739  
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn  
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787  
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile  
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 230 235 240

tgc 843

&lt;210&gt; 882

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 882

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile  
 1 5 10 15

Ala	Leu	Val	Met	Ala	Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	20	25	30
Gln	Leu	Thr	Pro	Leu	Asn	Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	35	40	45
Phe	Leu	Gly	Gly	Glu	Gly	Gln	Trp	Leu	Leu	Ala	Met	Pro	Ala	His	His	50	55	60
Ile	Ala	Gly	Met	Gln	Val	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	65	70	75
Pro	Leu	Ala	Ile	Asp	Leu	Ser	Thr	Gly	Phe	His	Ile	Asp	Ala	Phe	Ala	85	90	95
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser	100	105	110
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile	115	120	125
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu	130	135	140
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val	145	150	155
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly	165	170	175
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu	180	185	190
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His	195	200	205
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu	210	215	220
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His	225	230	235

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<210> 883
<211> 384
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(361)  
<223> RXS02908
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<400> 883  
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gtgactggtc gcgtggatac ccgtcattga ttccgggtgga ttg aag ttg cac cca 115  
Leu Lys Leu His Pro



	1	5	
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg			163
Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala			
	10	15	20
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc			211
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala			
	25	30	35
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac			259
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp			
	40	45	50
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct			307
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser			
	55	60	65
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag			355
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys			
	70	75	80
ctg ttt tagtcttcat tcttgctggc tgc			384
Leu Phe			

&lt;210&gt; 884

&lt;211&gt; 87

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 884

Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
1 5 10 15

Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
20 25 30

Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
35 40 45

Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
50 55 60

Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
65 70 75 80

Arg Ala Ile Ala Lys Leu Phe
85

&lt;210&gt; 885

&lt;211&gt; 705

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(682)

&lt;223&gt; RXA00997

&lt;400&gt; 885

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ccccatctgtg gcagatcgaa tgcacccacc gcggagaagt cgtcgcacga accacactgc 60

gcaccatggt gctgaacaag tagccctata ctcgggcacc atg act aca tgg aaa 115
                                   Met Thr Thr Trp Lys
                                   1 5

gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
                                   10 15 20

tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
                                   25 30 35

ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
                                   40 45 50

tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
                                   55 60 65

gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
                                   70 75 80 85

gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
                                   90 95 100

atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
                                   105 110 115

ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499
Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
                                   120 125 130

cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
                                   135 140 145

cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
                                   150 155 160 165

ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
                                   170 175 180

caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692
Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
                                   185 190

atcttgcacc tga 705

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&lt;210&gt; 886

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 886

Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu  
 1 5 10 15

Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile  
 20 25 30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys  
 35 40 45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser  
 50 55 60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile  
 65 70 75 80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp  
 85 90 95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser  
 100 105 110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala  
 115 120 125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile  
 130 135 140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val  
 145 150 155 160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp  
 165 170 175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr  
 180 185 190

Lys Lys

&lt;210&gt; 887

&lt;211&gt; 861

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(838)

&lt;223&gt; RXA02189

&lt;400&gt; 887

aatggcaaaa atgggcacat acgatactga tgggaccaat gggaaaacct caagccacca 60

attgagccag ttctctcaag caaaccgata ctggtgggat gtg gac gcg gcc gac 115  
 Val Asp Ala Ala Asp  
 1 5

tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc	163
Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly	
10 15 20	
gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt	211
Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu	
25 30 35	
ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt	259
Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly	
40 45 50	
tgc ggc tcg gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat	307
Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn	
55 60 65	
gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca	355
Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala	
70 75 80 85	
ggc cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc	403
Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu	
90 95 100	
ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc	451
Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala	
105 110 115	
atc ccc ttt gtg gag gat tcc gcc gca ctc atg aag gaa atc gcg cgc	499
Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg	
120 125 130	
gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg	547
Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met	
135 140 145	
cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc	595
Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile	
150 155 160 165	
acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc	643
Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr	
170 175 180	
ggc gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg cgg atc	691
Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile	
185 190 195	
aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca	739
Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro	
200 205 210	
gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt	787
Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly Gln Trp Ser Pro Leu	
215 220 225	
cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc	835
Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg	
230 235 240 245	
ccc taataaacca acggcgctca ttt	861

Pro

&lt;210&gt; 888

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 888

Val	Asp	Ala	Ala	Asp	Tyr	His	Glu	Arg	His	Pro	Ser	Tyr	Leu	Gly	Thr
1				5					10					15	

Asp	Ser	Ala	His	Gly	Glu	Phe	Tyr	Trp	Cys	Pro	Glu	Met	Leu	His	Glu
			20					25					30		

Lys	Asp	Val	Arg	Leu	Leu	Gly	Thr	Pro	Ala	Ala	Leu	Ser	Gly	Lys	Lys
		35					40					45			

Ile	Leu	Glu	Ile	Gly	Cys	Gly	Ser	Ala	Pro	Cys	Ala	Arg	Trp	Leu	Ala
50						55					60				

Asn	Asp	Val	Pro	Asn	Ala	Phe	Val	Thr	Ala	Phe	Asp	Ile	Ser	Ser	Gln
65					70					75					80

Met	Leu	Lys	Tyr	Ala	Gly	His	Asp	His	Asn	Val	His	Leu	Val	Gln	Ala
				85					90					95	

Asp	Ala	Met	Ser	Leu	Pro	Tyr	Ala	Asp	Ser	Ser	Phe	Asp	Val	Val	Phe
			100					105					110		

Ser	Val	Phe	Gly	Ala	Ile	Pro	Phe	Val	Glu	Asp	Ser	Ala	Ala	Leu	Met
		115					120					125			

Lys	Glu	Ile	Ala	Arg	Val	Leu	Lys	Pro	Gly	Gly	Arg	Leu	Ile	Phe	Ser
	130					135					140				

Ile	Thr	His	Pro	Met	Arg	Trp	Ile	Phe	Leu	Asp	Asp	Pro	Gly	Pro	Ala
145					150					155					160

Gly	Leu	Thr	Ala	Ile	Thr	Ser	Tyr	Phe	Asp	Gln	Arg	Gly	Tyr	Val	Glu
			165						170					175	

Glu	Asp	Glu	Glu	Thr	Gly	Ala	Leu	Ser	Tyr	Ala	Glu	Gln	His	Arg	Thr
		180						185					190		

Met	Gly	Ala	Arg	Ile	Asn	Glu	Leu	Ile	Asp	Ala	Ser	Leu	His	Leu	Asp
		195					200					205			

His	Leu	Ile	Glu	Pro	Glu	Trp	Pro	Asp	Glu	Leu	Glu	Glu	Asn	Trp	Gly
	210					215					220				

Gln	Trp	Ser	Pro	Leu	Arg	Gly	Lys	Leu	Phe	Pro	Gly	Thr	Ala	Ile	Phe
225					230					235					240

Leu	Ala	Thr	Tyr	Arg	Pro
					245

&lt;210&gt; 889

&lt;211&gt; 813

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(790)

&lt;223&gt; RXA02311

&lt;400&gt; 889

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cattttgggt atcggttggg tgtccatcgg tggagctaag ggcgctaagc atcgcagcca 60

aataacctcc cactaaagct cctggggttag actcgaacgc gtg gct aaa gca gat 115
                                   Val Ala Lys Ala Asp
                                   1 5

tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163
Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly
                                   10 15 20

aag aac tac gat ctc acc aat acc gtg ctt tct ttt ggt cag gac cgt 211
Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg
                                   25 30 35

gtg tgg cga aag cgc act agg cag cgc ctg gac ctc aag cca ggg gag 259
Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu
                                   40 45 50

aag gtg ctt gat cta gct gca gga aca gcc gtt tcc acc gtg gag ttg 307
Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu
                                   55 60 65

gca aaa tcc ggc gcg ttt tgt gtg gcg tgt gat ttc tcc cag ggc atg 355
Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met
                                   70 75 80 85

ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403
Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly
                                   90 95 100

atg cag ttg ccg ttt gca gac aac agc ttt gat gct gtg acc att tct 451
Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp Ala Val Thr Ile Ser
                                   105 110 115

tat ggt ctg cgc aat att cac gat ttc cgc gct ggc ctg aaa gaa atg 499
Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala Gly Leu Lys Glu Met
                                   120 125 130

gcc cgc gtg act aaa cct ggt gga cgc ctc acc gtg gcg gag ttc tcc 547
Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr Val Ala Glu Phe Ser
                                   135 140 145

acc ccc gtg atc cct gtg ttc ggc acc gtg tac aag gag tac ctc atg 595
Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr Lys Glu Tyr Leu Met
                                   150 155 160 165

cgc ctg ctg ccc cag gcg gcg cgc gca gta tgc tcc aac ccg gag gcc 643
Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser Ser Asn Pro Glu Ala
                                   170 175 180

tac att tac ctg gct gat tcc atc cgc gca tgg cct agc cag gcg gaa 691
Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp Pro Ser Gln Ala Glu

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185 190 195  
 cta gca cgg gag atc aac cag aat ggt tgg tca gat tgc ggt tgg cag 739  
 Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser Asp Cys Gly Trp Gln  
 200 205 210  
 aac ctg acc ttc ggc atc gtc gcg ctg cac tcg gcg att aaa cca gag 787  
 Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser Ala Ile Lys Pro Glu  
 215 220 225  
 aac tagtcgagtc ccacagaggg gag 813  
 Asn  
 230  
 <210> 890  
 <211> 230  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
 <400> 890  
 Val Ala Lys Ala Asp Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met  
 1 5 10 15  
 Phe Asp Asp Val Gly Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser  
 20 25 30  
 Phe Gly Gln Asp Arg Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp  
 35 40 45  
 Leu Lys Pro Gly Glu Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val  
 50 55 60  
 Ser Thr Val Glu Leu Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp  
 65 70 75 80  
 Phe Ser Gln Gly Met Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys  
 85 90 95  
 Val Val Gly Asp Gly Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp  
 100 105 110  
 Ala Val Thr Ile Ser Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala  
 115 120 125  
 Gly Leu Lys Glu Met Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr  
 130 135 140  
 Val Ala Glu Phe Ser Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr  
 145 150 155 160  
 Lys Glu Tyr Leu Met Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser  
 165 170 175  
 Ser Asn Pro Glu Ala Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp  
 180 185 190  
 Pro Ser Gln Ala Glu Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser  
 195 200 205  
 Asp Cys Gly Trp Gln Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser

210

215

220

Ala Ile Lys Pro Glu Asn  
225 230

<210> 891  
<211> 876  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(853)  
<223> RXN02912

<400> 891  
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gatattgaaa tgacgtattc ctgattgggc tgaaaaatct gtg aca tca cct gaa 115  
Val Thr Ser Pro Glu  
1 5  
tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac 163  
Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly Arg Ala Glu Ala Tyr  
10 15 20  
cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc 211  
His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln Phe Glu Arg Pro Ile  
25 30 35  
tgg gaa aag gtg tgg tcg aag gct ttg cct atc gtg tcg gaa gaa gcg 259  
Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile Val Ser Glu Glu Ala  
40 45 50  
gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt 307  
Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly Tyr Val Thr His Leu  
55 60 65  
cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa 355  
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu  
70 75 80 85  
atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tcg acg ggt 403  
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly  
90 95 100  
cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc 451  
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe  
105 110 115  
cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act 499  
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr  
120 125 130  
ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa 547  
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys  
135 140 145  
cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc 595  
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly



150	155	160	165	
att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc				643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe				
	170	175	180	
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg				691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr				
	185	190	195	
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc				739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu				
	200	205	210	
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag				787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln				
	215	220	225	
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc				835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe				
	230	235	240	245
agg gga att aaa tcc agt tagtgctgtt ttaagcggtc gag				876
Arg Gly Ile Lys Ser Ser				
	250			

&lt;210&gt; 892

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 892

Val Thr Ser Pro Glu Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly				
1	5	10	15	
Arg Ala Glu Ala Tyr His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln				
	20	25	30	
Phe Glu Arg Pro Ile Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile				
	35	40	45	
Val Ser Glu Glu Ala Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly				
	50	55	60	
Tyr Val Thr His Leu Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val				
	65	70	75	80
Asp Gly Ser Glu Glu Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu				
	85	90	95	
Arg Arg Ser Thr Gly Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala				
	100	105	110	
His Asp Pro Glu Phe Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg				
	115	120	125	
Tyr Val Leu Trp Thr Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp				
	130	135	140	
Val Ser Leu Leu Lys Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala				

145	150	155	160
Trp Tyr Pro Lys Gly Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp			
	165	170	175
Gly Pro Ser Ala Phe Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn			
	180	185	190
Leu Pro Met Ser Thr Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe			
	195	200	205
His Asn Ala Gly Leu Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu			
	210	215	220
Ala Glu Leu Asp Gln Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr			
	225	230	235
Pro Gln Phe Leu Phe Arg Gly Ile Lys Ser Ser			
	245	250	

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 <211> 585  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXS00998

<400> 893  
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tgaaaatcca accatttttag gccgactaga gtaattaatt atg act tcc cgc gat 115  
 Met Thr Ser Arg Asp  
 1 5

gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga 163  
 Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg  
 10 15 20

gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211  
 Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly  
 25 30 35

ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg 259  
 Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg  
 40 45 50

gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307  
 Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly  
 55 60 65

ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355  
 Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser  
 70 75 80 85

gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac 403  
 Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn  
 90 95 100

aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451  
 Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala  
                   105                                  110                                  115

gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499  
 Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile  
                   120                                  125                                  130

gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547  
 Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr  
                   135                                  140                                  145

atg gtg ctg aac aag tagccctata ctcgggcacc atg 585  
 Met Val Leu Asn Lys  
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<210> 894

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 894

Met Thr Ser Arg Asp Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu  
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Leu Ala Ala Thr Arg Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn  
                   20                                  25                                  30

Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr  
                   35                                  40                                  45

Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His  
           50                                  55                                  60

Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala  
           65                                  70                                  75                                  80

Glu Ser Thr Gly Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met  
                   85                                  90                                  95

Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser  
                   100                                  105                                  110

Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr  
                   115                                  120                                  125

His Leu Trp Gln Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg  
           130                                  135                                  140

Thr Thr Leu Arg Thr Met Val Leu Asn Lys  
 145                                  150

<210> 895

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

&lt;221&gt; CDS

&lt;222&gt; (101)..(1075)

&lt;223&gt; RXA01215

&lt;400&gt; 895

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cccaaaacgt ccacaaccag gaaggctaag caggatcctc atg act gct cac tgg 115  
 Met Thr Ala His Trp  
 1 5

aaa caa aac caa aag aac ctc atg ctg ttt tcg ggt cgt gcg cac cca 163  
 Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro  
 10 15 20

gaa ctg gca gaa gct gta gct aaa gag ctc gac gtc aac gtc acc cca 211  
 Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro  
 25 30 35

atg acg gca cgc gat ttc gcc aac ggt gaa atc tac gtc cgc ttc gag 259  
 Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu  
 40 45 50

gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag 307  
 Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln  
 55 60 65

cct ctc aac aag tgg ctc atg gaa cag ctg ctg atg atc gac gct ttg 355  
 Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu Met Ile Asp Ala Leu  
 70 75 80 85

aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca 403  
 Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro  
 90 95 100

tat gcc cgc cag gac aag aag cac cgc ggc cgc gag cca att tct gct 451  
 Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala  
 105 110 115

cgc ctc atc gcc gac ctc atg ctc acc gct ggc gcg gac cgt atc gtg 499  
 Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly Ala Asp Arg Ile Val  
 120 125 130

tcc gtg gac ttg cac acc gat cag atc cag ggc ttc ttc gac ggc cca 547  
 Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly Phe Phe Asp Gly Pro  
 135 140 145

gtc gat cac atg cac gcc atg ccg atc ctc acc gat cac atc aag gaa 595  
 Val Asp His Met His Ala Met Pro Ile Leu Thr Asp His Ile Lys Glu  
 150 155 160 165

aac tac aac ctg gac aac atc tgc gtg gtc tcc cct gac gca ggt cgc 643  
 Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser Pro Asp Ala Gly Arg  
 170 175 180

gtg aag gtt gca gag aag tgg gct aac acc ttg ggc gat gcc cca atg 691  
 Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu Gly Asp Ala Pro Met  
 185 190 195

gcg ttc gtg cac aag acc cgc tcc acc gag gta gca aac cag gtt gtc 739  
 Ala Phe Val His Lys Thr Arg Ser Thr Glu Val Ala Asn Gln Val Val

200	205	210	
gcc aac cgc gtc gtc ggt gac gtc gac ggc aag gac tgc gtg ctt ctc			787
Ala Asn Arg Val Val Gly Asp Val Asp Gly Lys Asp Cys Val Leu Leu			
215	220	225	
gac gac atg atc gac act ggc ggc acc atc gcc ggc gct gtg ggc gtc			835
Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala Gly Ala Val Gly Val			
230	235	240	245
ctg aag aag gct ggc gca aag tca gtc gtc atc gcc tgc acc cac ggt			883
Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile Ala Cys Thr His Gly			
250	255		260
gtg ttc tct gac cca gcc cgc gag cgc ctg tct gca tgc ggt gct gaa			931
Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser Ala Cys Gly Ala Glu			
265	270		275
gaa gtc atc acc acc gac acc ctg cca cag tcc acc gag ggc tgg agc			979
Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser Thr Glu Gly Trp Ser			
280	285		290
aac ctg acc gtt ttg tgc atc gca ccg ctg ctg gct cgc acc atc aac			
1027			
Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu Ala Arg Thr Ile Asn			
295	300		305
gag atc ttc gaa aac ggt tcc gtc acc acc ctc ttc gag ggc gag gcc			
1075			
Glu Ile Phe Glu Asn Gly Ser Val Thr Thr Leu Phe Glu Gly Glu Ala			
310	315		320
325			
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1098			

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 896  
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 Gly Arg Ala His Pro Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp  
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 Val Asn Val Thr Pro Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile  
 35 40 45  
 Tyr Val Arg Phe Glu Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu  
 50 55 60  
 Gln Ser His Thr Gln Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu  
 65 70 75 80  
 Met Ile Asp Ala Leu Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile  
 85 90 95  
 Leu Pro Phe Tyr Pro Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg

100	105	110
Glu Pro Ile Ser Ala Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly 115	120	125
Ala Asp Arg Ile Val Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly 130	135	140
Phe Phe Asp Gly Pro Val Asp His Met His Ala Met Pro Ile Leu Thr 145	150	155
Asp His Ile Lys Glu Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser 165	170	175
Pro Asp Ala Gly Arg Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu 180	185	190
Gly Asp Ala Pro Met Ala Phe Val His Lys Thr Arg Ser Thr Glu Val 195	200	205
Ala Asn Gln Val Val Ala Asn Arg Val Val Gly Asp Val Asp Gly Lys 210	215	220
Asp Cys Val Leu Leu Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala 225	230	235
Gly Ala Val Gly Val Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile 245	250	255
Ala Cys Thr His Gly Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser 260	265	270
Ala Cys Gly Ala Glu Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser 275	280	285
Thr Glu Gly Trp Ser Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu 290	295	300
Ala Arg Thr Ile Asn Glu Ile Phe Glu Asn Gly Ser Val Thr Thr Leu 305	310	315
Phe Glu Gly Glu Ala 325		

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN00558

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 Val Val Lys Lys Pro  
 1 5

gcg ggc atc gca gta ggc gat ggc gaa cag atc ctg gtt ttc aaa gat	163
Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp	
10 15 20	
ttg ggc cta gtc tcc caa gtt ttc gac caa cca att ctg gaa tcc ctc	211
Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu	
25 30 35	
cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga	259
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly	
40 45 50	
aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc	307
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly	
55 60 65	
acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag	355
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu	
70 75 80 85	
ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag	403
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys	
90 95 100	
cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat	451
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His	
105 110 115	
gac gga aat aat ctc ttt gat tcc gcc aag gaa ctc ctc ccc agc gtc	499
Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val	
120 125 130	
aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca	547
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala	
135 140 145	
gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag	595
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu	
150 155 160 165	
cgc ggc tgg gta gtc gca tct gaa acc gca gcg ctc gac atc gta ggt	643
Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
170 175 180	
gcc tcg cat gtg cgc gag gtc gaa cca ggc gaa ctg att gct atc gac	691
Ala Ser His Val Arg Glu Val Glu Pro Gly Glu Leu Ile Ala Ile Asp	
185 190 195	
gaa tcc ggc ctc aag tcc gca cga ttc gcc gag aca acc cgc aaa ggt	739
Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
200 205 210	
tgc gtc ttc gaa tac gtt tac ctg gct cgt cca gac tcc gtg atc aag	787
Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	

gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca 883  
 Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser  
 250 255 260

ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc 931  
 Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe  
 265 270 275

ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag 979  
 Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln  
 280 285 290

cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca  
 1027  
 Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro  
 295 300 305

ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc  
 1075  
 Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser  
 310 315 320 325

atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa  
 1123  
 Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile Arg Met Leu Arg Glu  
 330 335 340

gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa  
 1171  
 Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys  
 345 350 355

tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att  
 1219  
 Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile  
 360 365 370

gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc  
 1267  
 Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val  
 375 380 385

cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc  
 1315  
 Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser  
 390 395 400 405

atg gtt gca gca acc gag caa cca gcc aac gaa ctc tgc atc gcc tgc  
 1363  
 Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu Leu Cys Ile Ala Cys  
 410 415 420

ttc gac ggc aaa tac ccc atg ggt ctg cca cag gga aac agc aac gca  
 1411  
 Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln Gly Asn Ser Asn Ala  
 425 430 435

gac cta gtc cgc aag atg caa gca acc gcc tca agt taagatcggg  
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 440 445



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1470

<210> 898

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 898

Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile  
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Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro  
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Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr  
35 40 45

Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg  
50 55 60

Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu  
65 70 75 80

Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val  
85 90 95

Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu  
100 105 110

Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu  
115 120 125

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly  
130 135 140

His Thr Leu Tyr Ala Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser  
145 150 155 160

Ile Gly Arg Leu Glu Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala  
165 170 175

Leu Asp Ile Val Gly Ala Ser His Val Arg Glu Val Glu Pro Gly Glu  
180 185 190

Leu Ile Ala Ile Asp Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu  
195 200 205

Thr Thr Arg Lys Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro  
210 215 220

Asp Ser Val Ile Lys Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile  
225 230 235 240

Gly Arg Lys Leu Ala Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile  
245 250 255

Pro Thr Pro Glu Ser Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala  
260 265 270

Ser Gly Ile Pro Phe Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly  
 275 280 285  
 Arg Thr Phe Ile Gln Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg  
 290 295 300  
 Leu Lys Leu Asn Pro Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val  
 305 310 315 320  
 Val Val Asp Asp Ser Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile  
 325 330 335  
 Arg Met Leu Arg Glu Ala Gly Ala Ala Glu Val His Val Arg Ile Ala  
 340 345 350  
 Ser Pro Pro Val Lys Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr  
 355 360 365  
 Pro Gly Glu Leu Ile Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu  
 370 375 380  
 Met Val Glu Ala Val Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr  
 385 390 395 400  
 Val Ser Ile Asp Ser Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu  
 405 410 415  
 Leu Cys Ile Ala Cys Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln  
 420 425 430  
 Gly Asn Ser Asn Ala Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser  
 435 440 445

Ser

<210> 899  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (61)..(501)  
 <223> FRXA00558

<400> 899  
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 Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile  
 1 5 10 15

ctg gtt ttc aaa gat ttg ggc cta gtc tcc caa gtt ttc gac caa cca 156  
 Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro  
 20 25 30

att ctg gaa tcc ctc cgc gga aac atc gcc atc gga cac acc cga tac 204  
 Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr

35	40	45	
acc acc gcc ggc gga aac acc tgg gaa aat gcc cag cct atg ttc cgc			252
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
atg gca cca gat ggc acc gat atc gcc ctt gga cac aac ggc aac ctg			300
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
att aat tac atc gag ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc			348
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
gat ccc gcc aag aag cca tca gat acc gat gtg ctc act gga ctg ctc			396
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
gca agc ggc gtc cat gac gga aat aat ctc ttt gat tcc gcc aag gaa			444
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	
ctc ctc ccc agc gtc aag gga gcc tac tgc ctc acc ttc acc gac gga			492
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly			
130	135	140	
cac acc ctg taagcagcgc gtgatccatt cgg			524
His Thr Leu			
145			
<210> 900			
<211> 147			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 900			
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1	5	10	15
Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro			
20	25	30	
Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr			
35	40	45	
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly  
 130 135 140

His Thr Leu  
 145

<210> 901  
 <211> 1386  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1363)  
 <223> RXN00626

<400> 901  
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 aatagcttgg atcaagtttt gcaggataaa ctgtgcaacc atg cgc att ctg gta 115  
 Met Arg Ile Leu Val  
 1 5  
 atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act 163  
 Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr  
 10 15 20  
 gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt 211  
 Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu  
 25 30 35  
 gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag 259  
 Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu  
 40 45 50  
 gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc 307  
 Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile  
 55 60 65  
 ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg 355  
 Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala  
 70 75 80 85  
 gcg ggt atc gct gtg ttt ggt cct aac aag gac gct gct cgt atc gag 403  
 Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp Ala Ala Arg Ile Glu  
 90 95 100  
 ggc tcc aag gct ttc gct aag gat gtc atg gct gcg cag ggt gtt cgt 451  
 Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala Ala Gln Gly Val Arg  
 105 110 115  
 act gct cat gct gag act att act cct ggt gcg tct tct gaa gat att 499  
 Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala Ser Ser Glu Asp Ile  
 120 125 130  
 gat gct gcc ata gat cgt ttc ggc cca acg tgg gtt gtc aag gat gat 547  
 Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp  
 135 140 145  
 ggt ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca 595

Gly	Leu	Ser	Ala	Gly	Lys	Gly	Val	Val	Val	Thr	Pro	Asp	Arg	Ala	Ala		
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Ala	Arg	Ala	His	Val	Asp	Ala	Val	Leu	Glu	Gly	Gly	Asn	Pro	Val	Leu		
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ctg	gag	tcc	ttc	ctt	gat	ggc	cct	gag	gtt	tcc	ctg	ttc	tgc	ctg	gtt	691	
Leu	Glu	Ser	Phe	Leu	Asp	Gly	Pro	Glu	Val	Ser	Leu	Phe	Cys	Leu	Val		
			185					190					195				
gat	ggc	gag	acg	gta	gtt	cct	ctg	ctg	cca	gcg	cag	gat	cac	aag	cgt	739	
Asp	Gly	Glu	Thr	Val	Val	Pro	Leu	Leu	Pro	Ala	Gln	Asp	His	Lys	Arg		
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gcg	tac	gac	aac	gat	gag	ggc	cca	aac	act	ggt	ggc	atg	ggt	gct	tat	787	
Ala	Tyr	Asp	Asn	Asp	Glu	Gly	Pro	Asn	Thr	Gly	Gly	Met	Gly	Ala	Tyr		
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gcg	ccg	ctt	cct	tgg	ctg	cct	gaa	gat	ggc	gtc	cag	cgc	att	gtc	gat	835	
Ala	Pro	Leu	Pro	Trp	Leu	Pro	Glu	Asp	Gly	Val	Gln	Arg	Ile	Val	Asp		
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Glu	Val	Cys	Val	Pro	Val	Ala	Arg	Glu	Met	Val	Ala	Arg	Gly	Cys	Ala		
				250				255						260			
tac	tcc	ggt	ctg	ctt	tac	gca	ggt	atc	gca	tgg	ggt	gca	gaa	ggc	cct	931	
Tyr	Ser	Gly	Leu	Leu	Tyr	Ala	Gly	Ile	Ala	Trp	Gly	Ala	Glu	Gly	Pro		
			265					270					275				
gca	gta	gtg	gag	ttc	aac	tgc	cgc	ttc	ggc	gat	cca	gaa	acc	cag	gct	979	
Ala	Val	Val	Glu	Phe	Asn	Cys	Arg	Phe	Gly	Asp	Pro	Glu	Thr	Gln	Ala		
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gta	ctg	gca	cta	ctg	aag	act	cct	cta	gca	gta	ctg	ctc	aac	gca	gtt		
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Val	Leu	Ala	Leu	Leu	Lys	Thr	Pro	Leu	Ala	Val	Leu	Leu	Asn	Ala	Val		
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gct	act	gga	acc	ttg	gca	gag	cag	cca	gca	ctg	gag	tgg	gag	gat	gct		
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Ala	Thr	Gly	Thr	Leu	Ala	Glu	Gln	Pro	Ala	Leu	Glu	Trp	Glu	Asp	Ala		
310					315					320				325			
tac	gcc	ctg	act	gtg	gtg	ttg	gct	tct	tac	aac	tac	cca	gag	gca	cct		
1123																	
Tyr	Ala	Leu	Thr	Val	Val	Leu	Ala	Ser	Tyr	Asn	Tyr	Pro	Glu	Ala	Pro		
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cgt	act	ggt	gat	gtc	atc	cgc	aac	gct	gat	gca	gat	aac	gtt	ctt	cac		
1171																	
Arg	Thr	Gly	Asp	Val	Ile	Arg	Asn	Ala	Asp	Ala	Asp	Asn	Val	Leu	His		
			345					350					355				
gct	ggt	acc	gca	ctc	aat	gct	gaa	ggc	gag	ctg	gtc	tct	gcg	ggc	ggt		
1219																	
Ala	Gly	Thr	Ala	Leu	Asn	Ala	Glu	Gly	Glu	Leu	Val	Ser	Ala	Gly	Gly		
	360						365					370					

cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg gag gct gca cgc  
1267

Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu Glu Ala Ala Arg  
375 380 385

gat aac gcg tac acc acc atc aag gac att gaa ctt gag gga agc cac  
1315

Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu Glu Gly Ser His  
390 395 400 405

tac cgc agc gat atc gca ttg gct gca tta gag ggt cgt atc tcg atc  
1363

Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly Arg Ile Ser Ile  
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1386

<210> 902

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 902

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Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro  
20 25 30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys  
35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser  
50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala  
65 70 75 80

Asp Ala Leu Arg Ala Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp  
85 90 95

Ala Ala Arg Ile Glu Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala  
100 105 110

Ala Gln Gly Val Arg Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala  
115 120 125

Ser Ser Glu Asp Ile Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp  
130 135 140

Val Val Lys Asp Asp Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr  
145 150 155 160

Pro Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly  
165 170 175

Gly Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser  
180 185 190

Leu Phe Cys Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala  
 195 200 205  
 Gln Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly  
 210 215 220  
 Gly Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val  
 225 230 235 240  
 Gln Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val  
 245 250 255  
 Ala Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp  
 260 265 270  
 Gly Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp  
 275 280 285  
 Pro Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val  
 290 295 300  
 Leu Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu  
 305 310 315 320  
 Glu Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn  
 325 330 335  
 Tyr Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala  
 340 345 350  
 Asp Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu  
 355 360 365  
 Val Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr  
 370 375 380  
 Leu Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu  
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 Leu Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu  
 405 410 415  
 Gly Arg Ile Ser Ile  
 420

&lt;210&gt; 903

&lt;211&gt; 364

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(364)

&lt;223&gt; FRXA00629

&lt;400&gt; 903

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 Met Arg Ile Leu Val

	1	5	
atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act			163
Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr			
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gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt			211
Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu			
	25	30	35
gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag			259
Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu			
	40	45	50
gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc			307
Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile			
	55	60	65
ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg			355
Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala			
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gcg ggt atc			364
Ala Gly Ile			

&lt;210&gt; 904

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 904

Met Arg Ile Leu Val Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu
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Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro
20 25 30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
65 70 75 80

Asp Ala Leu Arg Ala Ala Gly Ile
85

&lt;210&gt; 905

&lt;211&gt; 803

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(780)

&lt;223&gt; FRXA00626



&lt;400&gt; 905

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Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly Gly	
1 5 10 15	
aat cca gtt ttg ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg	96
Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu	
20 25 30	
ttc ttc ctg gtt gat ggc gag acg gta gtt cct ctg ctg cca gcg cag	144
Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln	
35 40 45	
gat cac aag cgt gcg tac gac aac gat gag ggc cca aac act ggt ggc	192
Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly	
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Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln	
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cgc att gtc gat gag gtc tgc gtt cct gtt gct cgt gag atg gtg gca	288
Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala	
85 90 95	
cgt ggt tgc gcg tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt	336
Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly	
100 105 110	
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Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro	
115 120 125	
gaa acc cag gct gta ctg gca cta ctg aag act cct cta gca gta ctg	432
Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu	
130 135 140	
ctc aac gca gtt gct act gga acc ttg gca gag cag cca gca ctg gag	480
Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu	
145 150 155 160	
tgg gag gat gct tac gcc ctg act gtg gtg ttg gct tct tac aac tac	528
Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr	
165 170 175	
cca gag gca cct cgt act ggt gat gtc atc cgc aac gct gat gca gat	576
Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp	
180 185 190	
aac gtt ctt cac gct ggt acc gca ctc aat gct gaa ggc gag ctg gtc	624
Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val	
195 200 205	
tct gcg ggc ggt cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg	672
Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu	
210 215 220	
gag gct gca cgc gat aac gcg tac acc acc atc aag gac att gaa ctt	720
Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu	
225 230 235 240	

gag gga agc cac tac cgc agc gat atc gca ttg gct gca tta gag ggt 768  
 Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly  
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 Arg Ile Ser Ile  
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<212> PRT

<213> Corynebacterium glutamicum

<400> 906

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Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln  
                     35                    40                    45

Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly  
                     50                    55                    60

Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln  
   65                    70                    75                    80

Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala  
                     85                    90                    95

Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly  
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Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro  
                     115                    120                    125

Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu  
                     130                    135                    140

Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu  
   145                    150                    155                    160

Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr  
                     165                    170                    175

Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp  
                     180                    185                    190

Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val  
                     195                    200                    205

Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu  
                     210                    215                    220

Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu  
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Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly  
 245 250 255

Arg Ile Ser Ile  
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 <223> RXA02623

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 Val Asn Ser Asp Ser  
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 Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln  
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 Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser  
 25 30 35  
 gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259  
 Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp  
 40 45 50  
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 Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu  
 55 60 65  
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 70 75 80 85  
 gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403  
 Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser  
 90 95 100  
 cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451  
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala  
 105 110 115  
 cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499  
 His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser  
 120 125 130  
 aca gtt cac ctt gtc gat gct ggt gtg gat acc ggc cca att att gct 547  
 Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Ile Ile Ala  
 135 140 145  
 caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His  
 150 155 160 165

gaa aga atc aag cag gtt gag cgt aaa ctc att gta gaa gtc ctg aac 643  
 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn  
 170 175 180

agc gtg gaa ttt tcg cgt cag ggt ggc gta caa ctc aac tgg aga ggc 691  
 Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln Leu Asn Trp Arg Gly  
 185 190 195

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 <213> Corynebacterium glutamicum

<400> 908  
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Gly Thr Leu Leu Gln Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile  
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Val Gly Val Val Ser Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala  
 35 40 45

Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala  
 50 55 60

Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp  
 65 70 75 80

Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu  
 85 90 95

Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro  
 100 105 110

Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val  
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Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr  
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Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp  
 145 150 155 160

Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile  
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Leu Asn Trp Arg Gly  
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Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu His Ala Pro Ala His
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Gln Val Ala His Phe Ser Tyr Val Ile Asp Met Thr Asp Ala Ala Gln
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Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp Phe Val Ile Pro Glu
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Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys Ile Glu Glu Glu Gly
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cta gct acc atc gtg ccc act gca cgt gca gcc aag ctg acc atg aac 451
Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala Lys Leu Thr Met Asn
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Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro Val Met Ser Ser Ser
                               150                               155                               160                               165

ggc aag ggc caa tct gtt ttg cgt agt tca gac gat ctg cag gca gca 643
Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp Asp Leu Gln Ala Ala
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1027																	
Pro	His	Asp	Thr	Gly	Leu	Val	Thr	Leu	Ala	Thr	Gln	Arg	Phe	Ser	Glu		
	295					300					305						
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1123																	
Leu	Ile	Ser	Pro	Gly	Ala	Ser	Ala	Val	Ile	Tyr	Gly	Gly	Ile	Glu	Ser		
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gaa	ggc	gtg	agc	tac	acc	ggg	ttg	gct	gaa	gcg	ctg	gca	gtg	gct	gaa		
1171																	
Glu	Gly	Val	Ser	Tyr	Thr	Gly	Leu	Ala	Glu	Ala	Leu	Ala	Val	Ala	Glu		
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act	gat	ctt	cgt	atc	ttt	gcc	aag	cca	gag	gcc	ttc	acc	aag	cgt	cgc		
1219																	
Thr	Asp	Leu	Arg	Ile	Phe	Ala	Lys	Pro	Glu	Ala	Phe	Thr	Lys	Arg	Arg		
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atg	ggg	gtt	gca	gtg	tcc	acc	gct	gag	gat	gtg	gct	gca	gcc	agg	gac		
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Met	Gly	Val	Ala	Val	Ser	Thr	Ala	Glu	Asp	Val	Ala	Ala	Ala	Arg	Asp		
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cgc	gcc	act	ttg	gct	gcc	gcg	gcg	atc	aag	gtt	cat	cca	gga	aat	tcc		
1315																	
Arg	Ala	Thr	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Val	His	Pro	Gly	Asn	Ser		
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 Ala Glu Ala

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 <213> Corynebacterium glutamicum

<400> 910  
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                   20                  25                  30  
 Ala Phe Gln Arg Leu Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu  
           35                  40                  45  
 His Ala Pro Ala His Gln Val Ala His Phe Ser Tyr Val Ile Asp Met  
       50                  55                  60  
 Thr Asp Ala Ala Gln Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp  
   65                  70                  75                  80  
 Phe Val Ile Pro Glu Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys  
                   85                  90                  95  
 Ile Glu Glu Glu Gly Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala  
           100                  105                  110  
 Lys Leu Thr Met Asn Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu  
       115                  120                  125  
 Leu Gly Leu Pro Thr Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu  
       130                  135                  140  
 Phe Ser Ala Ala Ala Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro  
   145                  150                  155                  160  
 Val Met Ser Ser Ser Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp  
                   165                  170                  175  
 Asp Leu Gln Ala Ala Trp Asp Tyr Ala Met Ser Gly Ala Arg Val Ala  
           180                  185                  190  
 Asn Ser Arg Val Ile Val Glu Ala Phe Val Glu Phe Asp Tyr Glu Ile  
       195                  200                  205  
 Thr Leu Leu Thr Val Arg Ser Ile Asp Pro Thr Thr Ser Lys Pro Ala  
       210                  215                  220  
 Thr Trp Phe Cys Glu Pro Ile Gly His Arg Gln Glu Asp Gly Asp Tyr  
   225                  230                  235                  240  
 Val Glu Ser Trp Gln Pro Met Glu Met Thr Pro Arg Ala Leu Glu Asn  
           245                  250                  255

Ala Arg Ser Val Ala Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly  
 260 265 270

Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser  
 275 280 285

Glu Val Ser Pro Arg Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr  
 290 295 300

Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu  
 305 310 315 320

Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr  
 325 330 335

Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala  
 340 345 350

Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala  
 355 360 365

Phe Thr Lys Arg Arg Met Gly Val Ala Val Ser Thr Ala Glu Asp Val  
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Ala Ala Ala Arg Asp Arg Ala Thr Leu Ala Ala Ala Ala Ile Lys Val  
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His Pro Gly Asn Ser Ala Glu Ala  
 405

&lt;210&gt; 911

&lt;211&gt; 2409

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2386)

&lt;223&gt; RXN00537

&lt;400&gt; 911

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tgctccgccgt tggcaccatc gcggcttaag aggagtaa atg agc act ttt gtc 115  
 Met Ser Thr Phe Val  
 1 5

aat gac acc gtc gaa gac gca atc aag acc cct gag ctg gat cag cca 163  
 Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro Glu Leu Asp Gln Pro  
 10 15 20

ttt gag gct ctt ggt ctg aaa gac gac gag tac gcg cgc atc aag gaa 211  
 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu  
 25 30 35

atc ctt ggc cgc cgc cca acc gac gcc gag ctg acc gtt tac tcc gtc 259  
 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val  
 40 45 50

atg tgg tcg gag cac tgc tcc tac aag tcc tcc aag gtt cac ctg cgt 307



Met	Trp	Ser	Glu	His	Cys	Ser	Tyr	Lys	Ser	Ser	Lys	Val	His	Leu	Arg	
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Tyr	Phe	Gly	Glu	Thr	Thr	Thr	Glu	Glu	Met	Ala	Ser	Lys	Ile	Leu	Ala	85
70					75				80							
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Gly	Ile	Gly	Glu	Asn	Ala	Gly	Val	Val	Asp	Ile	Gly	Asp	Gly	Asn	Ala	100
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Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro	115
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His	Gln	Gly	Ala	Ala	Thr	Gly	Val	Gly	Gly	Ile	Val	Arg	Asp	Ile	Met	130
	120						125									
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Ala	Met	Gly	Ala	Arg	Pro	Ile	Ala	Val	Met	Asp	Gln	Leu	Arg	Phe	Gly	145
	135					140										
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Ala	Leu	Asp	Asn	Pro	Asp	Thr	Gln	Arg	Val	Phe	Pro	Gly	Val	Val	Asp	165
	150				155				160							
ggc	att	tcc	cat	tac	ggc	aac	tgc	ctc	ggc	ctg	cca	aac	atc	ggt	ggc	643
Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu	Gly	Leu	Pro	Asn	Ile	Gly	Gly	180
				170				175								
gaa	acc	gtc	ttc	gac	gat	tcc	tac	gca	ggt	aac	cca	ctg	gtc	aac	gca	691
Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn	Pro	Leu	Val	Asn	Ala	195
			185					190								
ctg	tgc	gtg	ggt	acc	ctc	aag	gtg	gaa	gac	ctc	aag	ctt	gca	ttc	gca	739
Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu	Lys	Leu	Ala	Phe	Ala	210
		200					205									
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Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly	Ser	Arg	Thr	Gly	Leu	225
	215				220											
gat	ggc	atc	ggt	ggc	gtg	tcc	gtc	ctg	ggt	tcc	gca	tcc	ttc	gaa	gaa	835
Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser	Ala	Ser	Phe	Glu	Glu	245
	230				235				240							
ggc	gaa	gag	cgc	aag	ctc	cca	gct	gtt	cag	gtt	ggc	gat	cct	ttc	gca	883
Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val	Gly	Asp	Pro	Phe	Ala	260
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Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu	Tyr	Lys	Ala	Gly	Val	275
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gtg	gtc	ggt	att	cag	gac	ctc	ggt	ggc	ggc	gga	ctt	gcg	tgt	gca	acc	979
Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly	Leu	Ala	Cys	Ala	Thr	290
		280					285									
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Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met Arg Val Asn Leu Asp  
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 aac gtc cca ctg cgc gca gag aac atg tct gca gct gaa atc ctg gct  
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 Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala Ala Glu Ile Leu Ala  
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 1123  
 Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val Thr Pro Glu Asn Val  
 330 335 340  
 gag cgt ttc ctc gag atc tgt gca aag tgg gat gtc acc tgc gca gaa  
 1171  
 Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp Val Thr Cys Ala Glu  
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 atc ggc gaa gtt acc gac gag aag gac cgc tac gtt gtg gtc cac aac  
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 Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr Val Val Val His Asn  
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 ggt gaa gtt gtt atc gac gca cct cca tca acc atc gat gaa ggc cct  
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 Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr Ile Asp Glu Gly Pro  
 375 380 385  
 gtc tac aac cgc cca gtt gct cgc cct gag aac cag gac gaa ctg cag  
 1315  
 Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn Gln Asp Glu Leu Gln  
 390 395 400 405  
 ctc gaa ggc gag atc gct cgc cca gtc gac gtt gaa gag atc aag gct  
 1363  
 Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val Glu Glu Ile Lys Ala  
 410 415 420  
 gct tgg ctg aag ctt gtc gct tca cca gca ctt gca tcc cgc gcg ttt  
 1411  
 Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu Ala Ser Arg Ala Phe  
 425 430 435  
 atc acc gag cag tac gac cgc tac gtc cgc ggc aac acc gtt cag gca  
 1459  
 Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly Asn Thr Val Gln Ala  
 440 445 450  
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 1507  
 Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr Asn Arg  
 455 460 465  
 ggc gtt gcg atc tcc gcc gac gca tcc ggc cgt tac acc aag ctc gag  
 1555  
 Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys Leu Glu  
 470 475 480 485  
 cca aac act ggc gcg cag ctt gca ctg gct gag gct tac cgc aac gtg  
 1603  
 Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg Asn Val

490										495					500					
gtc tcc acc ggt gca cgc cca gtg gct gtc acc aac tgc ctg aac ttc																				
1651																				
Val	Ser	Thr	Gly	Ala	Arg	Pro	Val	Ala	Val	Thr	Asn	Cys	Leu	Asn	Phe					
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ggt tcc cca gaa aac gct ggt gtt atg tgg cag ttc aag gaa gca gtc																				
1699																				
Gly	Ser	Pro	Glu	Asn	Ala	Gly	Val	Met	Trp	Gln	Phe	Lys	Glu	Ala	Val					
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cac ggt ctg gca gac gga tcc aag ctt ttg ggc att cca gtg tcc ggc																				
1747																				
His	Gly	Leu	Ala	Asp	Gly	Ser	Lys	Leu	Leu	Gly	Ile	Pro	Val	Ser	Gly					
	535					540				545										
ggt aac gtc tcc ttc tac aac cag act ggt gac gag ccc atc ctg cca																				
1795																				
Gly	Asn	Val	Ser	Phe	Tyr	Asn	Gln	Thr	Gly	Asp	Glu	Pro	Ile	Leu	Pro					
550					555					560					565					
acc cca gtc gtg ggt gtt ttg gga gtc ttg gac aac gtc gag cag agc																				
1843																				
Thr	Pro	Val	Val	Gly	Val	Leu	Gly	Val	Leu	Asp	Asn	Val	Glu	Gln	Ser					
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atc ggc aac gtc ctc cca tcc gag gac aac gat ctc tac ctc ctg ggt																				
1891																				
Ile	Gly	Asn	Val	Leu	Pro	Ser	Glu	Asp	Asn	Asp	Leu	Tyr	Leu	Leu	Gly					
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gag acc ttc gat gag ttc ggt ggc tcc atc tgg cag cag gtt tct ggc																				
1939																				
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gct ggc ctc aac ggt ctg cca cca gta gtt gac ctg ctc aac gag cag																				
1987																				
Ala	Gly	Leu	Asn	Gly	Leu	Pro	Pro	Val	Val	Asp	Leu	Leu	Asn	Glu	Gln					
	615					620				625										
cgt ctt gca gac ctg ttc gtc ggt tct gat ctg ttt gct gca tcc cac																				
2035																				
Arg	Leu	Ala	Asp	Leu	Phe	Val	Gly	Ser	Asp	Leu	Phe	Ala	Ala	Ser	His					
630					635					640					645					
gat ctg tct gag ggc ggc ctt ggc cag acc ctc gca gag ctt gcg atc																				
2083																				
Asp	Leu	Ser	Glu	Gly	Gly	Leu	Gly	Gln	Thr	Leu	Ala	Glu	Leu	Ala	Ile					
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cac cag aaa aag gga atg gat gtt gat ctc tcc cag atc cac cca tcc																				
2131																				
His	Gln	Lys	Lys	Gly	Met	Asp	Val	Asp	Leu	Ser	Gln	Ile	His	Pro	Ser					
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ctg ttc acc tca ctg ttt gct gag tcc gct tcc cgc atc gtg gtt gca																				
2179																				
Leu	Phe	Thr	Ser	Leu	Phe	Ala	Glu	Ser	Ala	Ser	Arg	Ile	Val	Val	Ala					
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acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt  
2227

Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val  
695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc  
2275

Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val  
710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa  
2323

Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu  
730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct  
2371

Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala  
745 750 755

aac gca gta gtt gca taattttctg ctgtgaagcc ggg  
2409

Asn Ala Val Val Ala  
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<210> 912

<211> 762

<212> PRT

<213> Corynebacterium glutamicum

<400> 912

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20 25 30

Ala Arg Ile Lys Glu Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu  
35 40 45

Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser  
50 55 60

Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala  
65 70 75 80

Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile  
85 90 95

Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro  
100 105 110

Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile  
115 120 125

Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp  
130 135 140

Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe

145		150		155		160
Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu	165			170		175
Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn	180		185		190	
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu	195		200		205	
Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly	210		215		220	
Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser	225	230		235		240
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val		245		250		255
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu	260		265		270	
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly	275		280		285	
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met	290	295		300		
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala	305	310		315		320
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val		325		330		335
Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp	340		345		350	
Val Thr Cys Ala Glu Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr	355		360		365	
Val Val Val His Asn Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr	370		375		380	
Ile Asp Glu Gly Pro Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn	385	390		395		400
Gln Asp Glu Leu Gln Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val		405		410		415
Glu Glu Ile Lys Ala Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu	420		425		430	
Ala Ser Arg Ala Phe Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly	435		440		445	
Asn Thr Val Gln Ala Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp	450		455		460	
Glu Glu Thr Asn Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg	465	470		475		480

Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu  
 485 490 495  
 Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr  
 500 505 510  
 Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln  
 515 520 525  
 Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly  
 530 535 540  
 Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp  
 545 550 555 560  
 Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp  
 565 570 575  
 Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp  
 580 585 590  
 Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp  
 595 600 605  
 Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp  
 610 615 620  
 Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu  
 625 630 635 640  
 Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu  
 645 650 655  
 Ala Glu Leu Ala Ile His Gln Lys Lys Gly Met Asp Val Asp Leu Ser  
 660 665 670  
 Gln Ile His Pro Ser Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser  
 675 680 685  
 Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala  
 690 695 700  
 Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser  
 705 710 715 720  
 Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val  
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 His Ala Val Gly Ala Asn Ala Val Val Ala  
 755 760

&lt;210&gt; 913

&lt;211&gt; 638

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (54) .. (638)  
 <223> FRXA02805

<400> 913

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                                     Val Phe
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Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
      5                                10                                15

cca aac atc ggt ggc gaa acc gtc ttc gac gat tcc tac gca ggt aac 155
Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
      20                                25                                30

cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
      35                                40                                45

aag ctt gca ttc gca tcc ggc acc ggc aac aag gtg atc ctg ttc ggt 251
Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
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tcc cgc acc ggc ctt gat ggc atc ggt ggc gtg tcc gtc ctg ggt tcc 299
Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
      70                                75                                80

gca tcc ttc gaa gaa ggc gaa gag cgc aag ctc cca gct gtt cag gtt 347
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
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ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
     100                                105                                110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
     115                                120                                125                                130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met
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cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
     150                                155                                160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
     165                                170                                175

acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635
Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp
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gtc
Val
195

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<210> 914  
 <211> 195  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 914

Val Phe Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu  
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Gly Leu Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala  
 20 25 30

Gly Asn Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu  
 35 40 45

Asp Leu Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu  
 50 55 60

Phe Gly Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu  
 65 70 75 80

Gly Ser Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val  
 85 90 95

Gln Val Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu  
 100 105 110

Glu Leu Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly  
 115 120 125

Gly Gly Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly  
 130 135 140

Gly Met Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met  
 145 150 155 160

Ser Ala Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala  
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Val Val Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys  
 180 185 190

Trp Asp Val  
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<210> 915  
 <211> 697  
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 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (23)..(697)

<223> FRXA00537

<400> 915

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 Val Tyr His Arg Ala Val Leu Asn Ala Thr



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Ser Ala Ala Thr Pro Phe Lys Gln Lys Asn Ala Asn Ala Gly Val Leu	15	20	25	
cgt atc gac gaa gag acc anc cgt ggc gtt gcg atc tcc gcc gac gca				148
Arg Ile Asp Glu Thr Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala	30	35	40	
tcc ggc cgt tac acc aag ctc gag cca aac act ggc gcg cag ctt gca				196
Ser Gly Arg Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala	45	50	55	
ctg gct gag gct tac cgc aac gtg gtc tcc acc ggt gca cgc cca gtg				244
Leu Ala Glu Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val	60	65	70	
gct gtc acc aac tgc ctg aac ttc ggt tcc cca gaa aac gct ggt gtt				292
Ala Val Thr Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val	75	80	85	90
atg tgg cag ttc aag gaa gca gtc cac ggt ctg gca gac gga tcc aag				340
Met Trp Gln Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys	95	100	105	
ctt ttg ggc att cca gtg tcc ggc ggt aac gtc tcc ttc tac aac cag				388
Leu Leu Gly Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln	110	115	120	
act ggt gac gag ccc atc ctg cca acc cca gtc gtg ggt gtt ttg gga				436
Thr Gly Asp Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly	125	130	135	
gtc ttg gac aac gtc gag cag agc atc ggc aac gtc ctc cca tcc gag				484
Val Leu Asp Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu	140	145	150	
gac aac gat ctc tac ctc ctg ggt gag acc ttc gat gag ttc ggt ggc				532
Asp Asn Asp Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly	155	160	165	170
tcc atc tgg cag cag gtt tct ggc gct ggc ctc aac ggt ctg cca cca				580
Ser Ile Trp Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro	175	180	185	
gta gtt gac ctg ctc aac gag cag cgt ctt gca gac ctg ttc gtc ggt				628
Val Val Asp Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly	190	195	200	
tct gat ctg ttt gct gca tcc cac gat ctg tct gag ggc ggc ctt ggc				676
Ser Asp Leu Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly	205	210	215	
cag acc ctc gca gag ctt gcg				697
Gln Thr Leu Ala Glu Leu Ala	220	225		

&lt;210&gt; 916

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 916

Val Tyr His Arg Ala Val Leu Asn Ala Thr Ser Ala Ala Thr Pro Phe  
 1 5 10 15

Lys Gln Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr  
 20 25 30

Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys  
 35 40 45

Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg  
 50 55 60

Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu  
 65 70 75 80

Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu  
 85 90 95

Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val  
 100 105 110

Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile  
 115 120 125

Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu  
 130 135 140

Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu  
 145 150 155 160

Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val  
 165 170 175

Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn  
 180 185 190

Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala  
 195 200 205

Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu  
 210 215 220

Ala

225

&lt;210&gt; 917

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(279)

&lt;223&gt; FRXA00561

&lt;400&gt; 917

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ctc ttc cca gat cca ccc atc cct gtt cac ctc act tgt ttg ctg agt 48
Leu Phe Pro Asp Pro Pro Ile Pro Val His Leu Thr Cys Leu Leu Ser
  1               5               10               15

ccc gct tcc cgc atc gtg gtt gca acc aac cgc ggc gaa gag ttg gaa 96
Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
      20               25               30

aag cgc gca gca gag ctg ggt gtt cca gtg ttc aag ctg ggc tgc acc 144
Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
      35               40               45

aac gat tca gcc gtc atc gct gtc aag ggc gca gac gtt gag ttc act 192
Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
      50               55               60

gtt tcc gtg gag gaa ctc cgc gaa gca tgg acc aac act ttg cct gag 240
Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
      65               70               75               80

gcc ttc ggt cac gca gtt gga gct aac gca gta gtt gca taattttctg 289
Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
      85               90

ctgtgaagcc ggg 302

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<210> 918  
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<400> 918
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Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
      20               25               30

Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
      35               40               45

Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
      50               55               60

Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
      65               70               75               80

Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
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<220>  
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 <223> RXA00541

&lt;400&gt; 919

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 Val Ser Ala Lys Ile  
 1 5

ggt gtc att acc ttc cca ggc acc ctt gac gat gta gat gca gca cgc 163  
 Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp Val Asp Ala Ala Arg  
 10 15 20

gct gct cgc atc gca ggt gca gaa gta atc agc ctg tgg cac gct gac 211  
 Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser Leu Trp His Ala Asp  
 25 30 35

gag gat ctc aag ggc gtc gac gca gtt gtc gtt ccc ggt gga ttc tcc 259  
 Glu Asp Leu Lys Gly Val Asp Ala Val Val Val Pro Gly Gly Phe Ser  
 40 45 50

tac ggc gat tac ctg cgc acc ggt gca atc tct gca ctg gcg cca gta 307  
 Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser Ala Leu Ala Pro Val  
 55 60 65

atg cag tcc gtg att gag cag gcc ggt aag ggt atg cca gtc ttg ggc 355  
 Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly Met Pro Val Leu Gly  
 70 75 80 85

att tgc aac ggc ttc cag atc ctc acc gaa gca cgc ctg ctt cca ggc 403  
 Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala Arg Leu Leu Pro Gly  
 90 95 100

gcg ctg acc cgc aac aag ggt ctg cac ttt cac tgt gta gac gca cac 451  
 Ala Leu Thr Arg Asn Lys Gly Leu His Phe His Cys Val Asp Ala His  
 105 110 115

ctc gtt gta gag aac aac acc act gca tgg acc aac act ttg gaa aag 499  
 Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr Asn Thr Leu Glu Lys  
 120 125 130

ggt cag cag atc ctt att cct gca aag cac ggt gaa ggt cgc ttc cag 547  
 Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly Glu Gly Arg Phe Gln  
 135 140 145

gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg 595  
 Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val  
 150 155 160 165

ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt 643  
 Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly  
 170 175 180

atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa 691  
 Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu  
 185 190 195

cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg 739  
 His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu  
 200 205 210

ttc ctg tcc gcc gtt ggc acc atc gcg gct taagaggagt aaatatgagc 789

Phe Leu Ser Ala Val Gly Thr Ile Ala Ala  
215 220

act

792

&lt;210&gt; 920

&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 920

Val Ser Ala Lys Ile Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp  
1 5 10 15

Val Asp Ala Ala Arg Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser  
20 25 30

Leu Trp His Ala Asp Glu Asp Leu Lys Gly Val Asp Ala Val Val Val  
35 40 45

Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser  
50 55 60

Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly  
65 70 75 80

Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala  
85 90 95

Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His  
100 105 110

Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr  
115 120 125

Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly  
130 135 140

Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly  
145 150 155 160

Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val  
165 170 175

Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu  
180 185 190

Met Pro His Pro Glu His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile  
195 200 205

Asp Gly Leu Glu Leu Phe Leu Ser Ala Val Gly Thr Ile Ala Ala  
210 215 220

&lt;210&gt; 921

&lt;211&gt; 1014

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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 <222> (101)..(991)  
 <223> RXA00620

<400> 921

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aattttccga acacacccga ggggtctaga cttgcctaac atg cgt cct gaa ctc 115
Met Arg Pro Glu Leu
1 5

tcc cag tac aag cac ctg tcg gca ggc aag gtc cgt gag atc tac gag 163
Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu
10 15 20

atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211
Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala
25 30 35

tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259
Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu
40 45 50

act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307
Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His
55 60 65

ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355
Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly
70 75 80 85

cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403
Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val
90 95 100

gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451
Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr
105 110 115

agc tcc gtg tgt gga gtt gag ctc cca gaa ggc ctc gtt gaa tct tct 499
Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser
120 125 130

cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547
Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly
135 140 145

gac cac gac atc aat gtc tcc ttt gac gtt gtt gaa gaa cgt ctc ggc 595
Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly
150 155 160 165

gaa gct cgt gcg aac cag ttg cgc gat gcc tct att gct att tac aag 643
Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys
170 175 180

gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691
Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val Ile Leu Ala Asp Thr
185 190 195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739
Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp

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200	205	210	
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Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp Pro Leu Glu Gly Tyr			
215	220	225	
gaa gca gga tct gtg caa cca agc ttt gat aag caa ttc gtg cgc aac			835
Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn			
230	235	240	245
tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag			883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu			
250	255		260
cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac			931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr			
265	270		275
atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att			979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile			
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1014			
Gly Ser Cys Val			
295			
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Arg Glu Ile Tyr Glu Ile Asp Asp Lys His Ile Leu Met Val Ala Ser			
20	25		30
Asp Arg Ile Ser Ala Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp			
35	40		45
Lys Gly Arg Val Leu Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile			
50	55		60
Asp Phe Pro Asn His Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro			
65	70	75	80
Glu Glu Val Leu Gly Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu			
85	90		95
Pro Phe Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val			
100	105		110
Glu Tyr Lys Gln Thr Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly			
115	120		125
Leu Val Glu Ser Ser Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr			
130	135		140

Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val  
 145 150 155 160  
 Glu Glu Arg Leu Gly Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser  
 165 170 175  
 Ile Ala Ile Tyr Lys Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val  
 180 185 190  
 Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr  
 195 200 205  
 Leu Val Leu Gly Asp Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp  
 210 215 220  
 Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys  
 225 230 235 240  
 Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys  
 245 250 255  
 Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala  
 260 265 270  
 Thr Arg Glu Arg Tyr Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys  
 275 280 285  
 Phe Cys Gln Trp Ile Gly Ser Cys Val  
 290 295

&lt;210&gt; 923

&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1270)

&lt;223&gt; RXN00770

&lt;400&gt; 923

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 Leu Leu Ser Pro Tyr  
 1 5  
 gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163  
 Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys  
 10 15 20  
 ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211  
 Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln  
 25 30 35  
 gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259  
 Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile  
 40 45 50  
 gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307



Glu	Ala	Gly	Asp	Arg	Ala	Val	Glu	Leu	Phe	Ala	Pro	Met	Ala	Lys	Arg		
55						60					65						
gcc	acc	cgc	cca	gag	gtt	ctt	ggc	aac	ctc	gga	ggc	ttc	gca	gga	ctc	355	
Ala	Thr	Arg	Pro	Glu	Val	Leu	Gly	Asn	Leu	Gly	Gly	Phe	Ala	Gly	Leu		
70					75				80						85		
ttt	gag	ctc	gga	aaa	tac	aag	aag	cca	atc	ctc	gca	gca	gga	tct	gac	403	
Phe	Glu	Leu	Gly	Lys	Tyr	Lys	Lys	Pro	Ile	Leu	Ala	Ala	Gly	Ser	Asp		
				90				95						100			
gga	gtc	ggc	acc	aag	ctt	gtc	atc	gcc	cag	atg	atg	gac	aag	cac	gac	451	
Gly	Val	Gly	Thr	Lys	Leu	Val	Ile	Ala	Gln	Met	Met	Asp	Lys	His	Asp		
			105					110						115			
acc	atc	ggc	atc	gac	ctt	gtt	gca	atg	tgt	gtg	gat	gac	ctc	gtt	gtc	499	
Thr	Ile	Gly	Ile	Asp	Leu	Val	Ala	Met	Cys	Val	Asp	Asp	Leu	Val	Val		
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Thr	Gly	Ala	Glu	Pro	Leu	Phe	Leu	Gln	Asp	Tyr	Ile	Ala	Ile	Gly	Lys		
	135					140					145						
gtt	gtc	cca	gag	cac	gtt	gct	gag	atc	gtc	tcc	ggt	atc	gca	gaa	ggc	595	
Val	Val	Pro	Glu	His	Val	Ala	Glu	Ile	Val	Ser	Gly	Ile	Ala	Glu	Gly		
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tgt	gtc	cag	gca	ggc	tgt	gct	ctg	ctc	ggt	ggc	gaa	acc	gca	gaa	cac	643	
Cys	Val	Gln	Ala	Gly	Cys	Ala	Leu	Leu	Gly	Gly	Glu	Thr	Ala	Glu	His		
				170					175						180		
cca	ggt	gtt	atg	gaa	cca	gac	cac	tac	gat	gtc	tcc	gca	act	gca	gtc	691	
Pro	Gly	Val	Met	Glu	Pro	Asp	His	Tyr	Asp	Val	Ser	Ala	Thr	Ala	Val		
			185					190						195			
ggc	gtt	gtc	gaa	gca	gat	gaa	ctg	cta	gga	cca	gac	cgc	gtc	cgc	gca	739	
Gly	Val	Val	Glu	Ala	Asp	Glu	Leu	Leu	Gly	Pro	Asp	Arg	Val	Arg	Ala		
	200					205						210					
ggc	gac	gtc	ctc	atc	ggc	atg	gct	tcc	tcc	ggt	ctg	cac	tcc	aac	ggt	787	
Gly	Asp	Val	Leu	Ile	Gly	Met	Ala	Ser	Ser	Gly	Leu	His	Ser	Asn	Gly		
	215					220					225						
tac	tcc	ctg	gct	cgc	cac	gtc	ctc	ctg	gaa	aag	gca	ggc	ctg	gcg	ctt	835	
Tyr	Ser	Leu	Ala	Arg	His	Val	Leu	Leu	Glu	Lys	Ala	Gly	Leu	Ala	Leu		
230					235					240					245		
gac	gga	cac	atc	gaa	gaa	ctc	gga	cgc	acc	ctc	ggt	gaa	gaa	ctt	ctc	883	
Asp	Gly	His	Ile	Glu	Glu	Leu	Gly	Arg	Thr	Leu	Gly	Glu	Glu	Leu	Leu		
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gag	cca	acc	cgc	atc	tac	gcc	aag	gac	tgc	ctg	gca	ctg	atc	gca	gag	931	
Glu	Pro	Thr	Arg	Ile	Tyr	Ala	Lys	Asp	Cys	Leu	Ala	Leu	Ile	Ala	Glu		
			265					270						275			
tgc	gaa	gtt	cac	acc	ttc	tgc	cac	gtc	acc	ggc	ggc	ggc	ctc	gca	ggc	979	
Cys	Glu	Val	His	Thr	Phe	Cys	His	Val	Thr	Gly	Gly	Gly	Leu	Ala	Gly		
	280						285						290				
aac	ctc	gag	cgg	gtt	gtc	cca	gaa	ggg	ctc	gtc	gca	gaa	atg	tcc	cga		
1027																	

Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val Ala Glu Met Ser Arg  
 295 300 305

gca act tgg acc cca ggc caa atc ttc cgc acc atc tcc tct gtg ggc  
 1075

Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly  
 310 315 320 325

aag gtt tcc cgc gaa gaa atg gaa aag acc ttc aac atg ggt gtc ggc  
 1123

Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly  
 330 335 340

atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg  
 1171

Met Val Ala Val Val Ala Glu Lys Asp Arg Asp Arg Ala Leu Ala Met  
 345 350 355

ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac  
 1219

Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn  
 360 365 370

ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc  
 1267

Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn Gly Glu His Pro Gly  
 375 380 385

tac taagcccaac tgtctgctct aag  
 1293

Tyr  
 390

<210> 924

<211> 390

<212> PRT

<213> Corynebacterium glutamicum

<400> 924

Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser  
 1 5 10 15

Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr  
 20 25 30

Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala  
 35 40 45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala  
 50 55 60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly  
 65 70 75 80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu  
 85 90 95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met  
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val  
 115 120 125  
 Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr  
 130 135 140  
 Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser  
 145 150 155 160  
 Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly  
 165 170 175  
 Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val  
 180 185 190  
 Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro  
 195 200 205  
 Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly  
 210 215 220  
 Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys  
 225 230 235 240  
 Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu  
 245 250 255  
 Gly Glu Glu Leu Leu Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu  
 260 265 270  
 Ala Leu Ile Ala Glu Cys Glu Val His Thr Phe Cys His Val Thr Gly  
 275 280 285  
 Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val  
 290 295 300  
 Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr  
 305 310 315 320  
 Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe  
 325 330 335  
 Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys Asp Arg Asp  
 340 345 350  
 Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile  
 355 360 365  
 Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn  
 370 375 380  
 Gly Glu His Pro Gly Tyr  
 385 390

&lt;210&gt; 925

&lt;211&gt; 818

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (15)..(818)

&lt;223&gt; FRXA00557

&lt;400&gt; 925

tggggttgagc atttttg ctc tcc ccg tat gcg tgg ggg ttg tcc cgc gca	50
Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala	
1 5 10	
ctt tta gac agt tat gtt cct aat aag ttc caa acc cca gca gga gaa	98
Leu Leu Asp Ser Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu	
15 20 25	
gcg aag tac acg atg agt gat cac cag gac acc acc gcc gaa ggc gtt	146
Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val	
30 35 40	
tca tac gca gca gca gga gtc gac atc gaa gcc ggc gat cgt gcc gtc	194
Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val	
45 50 55 60	
gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt	242
Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu	
65 70 75	
ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag	290
Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys	
80 85 90	
aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc	338
Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val	
95 100 105	
atc gcc cag atg atg gac aag cac gac acc atc ggc atc gac ctt gtt	386
Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val	
110 115 120	
gca atg tgt gtg gat gac ctc gtt gtc acc ggc gca gag cca ctg ttc	434
Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe	
125 130 135 140	
ctc cag gac tac atc gcc atc ggc aag gtt gtc cca gag cac gtt gct	482
Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala	
145 150 155	
gag atc gtc tcc ggt atc gca gaa ggc tgt gtc cag gca ggc tgt gct	530
Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala	
160 165 170	
ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac	578
Leu Leu Gly Gly Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp	
175 180 185	
cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa	626
His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu	
190 195 200	
ctg cta gga cca gac cgc gtc cgc gca ggc gac gtc ctc atc ggc atg	674
Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met	
205 210 215 220	

gct tcc tcc ggt ctg cac tcc aac ggt tac tcc ctg gct cgc cac gtc 722  
 Ala Ser Ser Gly Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val  
                   225                                  230                                  235

ctc ctg gaa aag gca ggc ctg gcg ctt gac gga cac atc gaa gaa ctc 770  
 Leu Leu Glu Lys Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu  
                   240                                  245                                  250

gga cgc acc ccc ggt gaa gaa ctt ctc gag cca acc cgc atg tac gcc 818  
 Gly Arg Thr Pro Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala  
                   255                                  260                                  265

<210> 926

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 926

Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser  
   1                                  5                                  10                                  15

Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr  
                   20                                  25                                  30

Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala  
                   35                                  40                                  45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala  
   50                                  55                                  60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly  
   65                                  70                                  75                                  80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu  
                   85                                  90                                  95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met  
                   100                                  105                                  110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val  
                   115                                  120                                  125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr  
                   130                                  135                                  140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser  
   145                                  150                                  155                                  160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly  
                   165                                  170                                  175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val  
                   180                                  185                                  190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro  
                   195                                  200                                  205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly  
   210                                  215                                  220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys  
 225 230 235 240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Pro  
 245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala  
 260 265

<210> 927

<211> 338

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(315)

<223> FRXA00770

<400> 927

gtc acc ggc ggc ggc ctc gca ggc aac ctc gag cgg gtt gtc cca gaa 48  
 Val Thr Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu  
 1 5 10 15

ggg ctc gtc gca gaa atg tcc cga gca act tgg acc cca ggc caa atc 96  
 Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile  
 20 25 30

ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa 144  
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu  
 35 40 45

aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag 192  
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys  
 50 55 60

gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc 240  
 Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys  
 65 70 75 80

tgg gaa atc gga acc gta cgc aac ggt gaa gag gga gag cct cgc gtg 288  
 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val  
 85 90 95

atc ctc aac ggc gag cac cct ggc tac taagcccaac tgtctgtctt 335  
 Ile Leu Asn Gly Glu His Pro Gly Tyr  
 100 105

aag 338

<210> 928

<211> 105

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 928

Val Thr Gly Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu  
 1 5 10 15

Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile  
                   20                                  25                                  30  
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu  
                   35                                  40                                  45  
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys  
                   50                                  55                                  60  
 Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys  
                   65                                  70                                  75                                  80  
 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val  
                   85                                  90                                  95  
 Ile Leu Asn Gly Glu His Pro Gly Tyr  
                   100                                  105

&lt;210&gt; 929

&lt;211&gt; 1320

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1297)

&lt;223&gt; RXN02345

&lt;400&gt; 929

accaccgacc ctatgtaatc aaccagggttc ccaaggctcg aaaagtggaa gcgctgctca 60  
 aagatcttac attttggtga aggcgttata gttaggactt gtg act tct aca gga 115  
   Val Thr Ser Thr Gly  
   1                                  5  
 aac caa gcc cac gct cca gga atg ccc atc gtc gca gta att ggt gac 163  
 Asn Gln Ala His Ala Pro Gly Met Pro Ile Val Ala Val Ile Gly Asp  
                                   10                                  15                                  20  
 ggc caa tta gcc cgc atg atg cag acc tcc gcc atc gaa ctc gga caa 211  
 Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala Ile Glu Leu Gly Gln  
                                   25                                  30                                  35  
 tca ctg cga gtt cta gct gga gcg ccg gat tcc tcc gca gct caa gta 259  
 Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser Ser Ala Ala Gln Val  
                                   40                                  45                                  50  
 gct gct gat gtt gtt ctc ggc gat tac acc aac att gat gat ctg cgc 307  
 Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn Ile Asp Asp Leu Arg  
                                   55                                  60                                  65  
 gtc gcc atc gaa ggc gcc gat gtg atg acc ttc gac cac gag cac gtc 355  
 Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe Asp His Glu His Val  
                                   70                                  75                                  80                                  85  
 ccc aac gaa cac ctg cac caa ctc atc gca gaa ggc gtc aac gtt cag 403  
 Pro Asn Glu His Leu His Gln Leu Ile Ala Glu Gly Val Asn Val Gln  
                                   90                                  95                                  100  
 cca cgc cca gaa gcg ctg gtc aac gca caa gac aaa ctt gtc atg cgc 451

Pro	Arg	Pro	Glu	Ala	Leu	Val	Asn	Ala	Gln	Asp	Lys	Leu	Val	Met	Arg		
			105					110					115				
aag	cgt	cta	cgt	gaa	ctc	ggc	gca	cca	gtc	cca	cca	ttt	gct	gcc	att	499	
Lys	Arg	Leu	Arg	Glu	Leu	Gly	Ala	Pro	Val	Pro	Pro	Phe	Ala	Ala	Ile		
		120					125					130					
gaa	tca	gtc	gaa	gat	gca	gtg	gga	ttc	ttc	gaa	gca	gtt	gat	ggc	caa	547	
Glu	Ser	Val	Glu	Asp	Ala	Val	Gly	Phe	Phe	Glu	Ala	Val	Asp	Gly	Gln		
		135				140					145						
gtt	tgc	ctc	aaa	gca	cgc	cgt	ggc	gga	tac	gac	ggc	aag	ggc	gta	tgg	595	
Val	Cys	Leu	Lys	Ala	Arg	Arg	Gly	Gly	Tyr	Asp	Gly	Lys	Gly	Val	Trp		
150					155					160					165		
ttc	cca	gcc	gat	gta	gca	gag	ctt	cag	tcg	ctt	gtg	gca	gag	ctt	ctc	643	
Phe	Pro	Ala	Asp	Val	Ala	Glu	Leu	Gln	Ser	Leu	Val	Ala	Glu	Leu	Leu		
				170					175					180			
gac	ggc	ggc	acc	cca	ctc	atg	gca	gaa	aag	aaa	gtt	gcc	ctc	aac	agg	691	
Asp	Gly	Gly	Thr	Pro	Leu	Met	Ala	Glu	Lys	Lys	Val	Ala	Leu	Asn	Arg		
			185					190					195				
gaa	ctg	tcc	gcc	atg	gtt	gcc	cgc	acc	cca	agt	gga	gaa	acc	aaa	gcg	739	
Glu	Leu	Ser	Ala	Met	Val	Ala	Arg	Thr	Pro	Ser	Gly	Glu	Thr	Lys	Ala		
		200					205					210					
tgg	cca	gtc	gta	gaa	tca	gtg	cag	aag	aac	ggg	gtg	tgt	gca	gaa	gca	787	
Trp	Pro	Val	Val	Glu	Ser	Val	Gln	Lys	Asn	Gly	Val	Cys	Ala	Glu	Ala		
		215				220					225						
atc	gct	ccc	gca	cct	gaa	cta	tcc	gca	gaa	ctg	cag	gaa	tcc	acc	aga	835	
Ile	Ala	Pro	Ala	Pro	Glu	Leu	Ser	Ala	Glu	Leu	Gln	Glu	Ser	Thr	Arg		
230					235					240					245		
gga	ttg	gcc	cag	aag	atc	gcc	acg	gaa	ctc	ggc	gtc	act	ggg	gtc	ttg	883	
Gly	Leu	Ala	Gln	Lys	Ile	Ala	Thr	Glu	Leu	Gly	Val	Thr	Gly	Val	Leu		
			250						255					260			
gca	gtg	gag	ctt	ttt	gaa	acc	ctc	gac	caa	aac	ggg	cag	cca	gag	atc	931	
Ala	Val	Glu	Leu	Phe	Glu	Thr	Leu	Asp	Gln	Asn	Gly	Gln	Pro	Glu	Ile		
			265					270					275				
ttt	gtc	aac	gag	ctc	gcc	atg	cgt	tca	cac	aac	acc	ggc	cac	tgg	act	979	
Phe	Val	Asn	Glu	Leu	Ala	Met	Arg	Ser	His	Asn	Thr	Gly	His	Trp	Thr		
		280					285					290					
caa	gat	ggc	tgc	gtg	acc	agc	caa	ttc	gag	cag	cac	ctc	cgc	gca	gtc		
1027																	
Gln	Asp	Gly	Cys	Val	Thr	Ser	Gln	Phe	Glu	Gln	His	Leu	Arg	Ala	Val		
		295				300					305						
ctc	gac	tac	cca	ctg	ggg	gct	acc	gac	act	ttg	gct	gat	tac	acc	gtg		
1075																	
Leu	Asp	Tyr	Pro	Leu	Gly	Ala	Thr	Asp	Thr	Leu	Ala	Asp	Tyr	Thr	Val		
310					315					320					325		
atg	gcc	aac	gtg	ctc	ggg	gcc	gac	acc	gac	cca	gag	atg	ccc	atg	gca		
1123																	
Met	Ala	Asn	Val	Leu	Gly	Ala	Asp	Thr	Asp	Pro	Glu	Met	Pro	Met	Ala		
			330						335					340			



acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac  
1171

Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His  
345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac  
1219

Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn  
360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc  
1267

Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys  
375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgcta  
1317

Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
390 395

gca  
1320

<210> 930

<211> 399

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 930

Val Thr Ser Thr Gly Asn Gln Ala His Ala Pro Gly Met Pro Ile Val  
1 5 10 15

Ala Val Ile Gly Asp Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala  
20 25 30

Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser  
35 40 45

Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn  
50 55 60

Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe  
65 70 75 80

Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu  
85 90 95

Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp  
100 105 110

Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro  
115 120 125

Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu  
130 135 140

Ala Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp  
145 150 155 160

Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu  
 165 170 175  
 Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys  
 180 185 190  
 Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser  
 195 200 205  
 Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly  
 210 215 220  
 Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu  
 225 230 235 240  
 Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly  
 245 250 255  
 Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn  
 260 265 270  
 Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn  
 275 280 285  
 Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln  
 290 295 300  
 His Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu  
 305 310 315 320  
 Ala Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro  
 325 330 335  
 Glu Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro  
 340 345 350  
 Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys  
 355 360 365  
 Ile Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala  
 370 375 380  
 Glu Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
 385 390 395

&lt;210&gt; 931

&lt;211&gt; 833

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(810)

&lt;223&gt; FRXA02345

&lt;400&gt; 931

ttt gct gcc att gaa tca gtc gaa gat gca gtg gga ttc ttc gaa gca 48  
 Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala  
 1 5 10 15

gtt gat ggc caa gtt tgc ctc aaa gca cgc cgt ggc gga tac gac ggc	96
Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly	
20 25 30	
aag ggc gta tgg ttc cca gcc gat gta gca gag ctt cag tcg ctt gtg	144
Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val	
35 40 45	
gca gag ctt ctc gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt	192
Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val	
50 55 60	
gcc ctc aac agg gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga	240
Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly	
65 70 75 80	
gaa acc aaa gcg tgg cca gtc gta gaa tca gtg cag aag aac ggt gtg	288
Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val	
85 90 95	
tgt gca gaa gca atc gct ccc gca cct gaa cta tcc gca gaa ctg cag	336
Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln	
100 105 110	
gaa tcc acc aga gga ttg gcc cag aag atc gcc acg gaa ctc ggc gtc	384
Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val	
115 120 125	
act ggt gtc ttg gca gtg gag ctt ttt gaa acc ctc gac caa aac ggg	432
Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly	
130 135 140	
cag cca gag atc ttt gtc aac gag ctc gcc atg cgt tca cac aac acc	480
Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr	
145 150 155 160	
ggc cac tgg act caa gat ggc tgc gtg acc agc caa ttc gag cag cac	528
Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His	
165 170 175	
ctc cgc gca gtc ctc gac tac cca ctg ggt gct acc gac act ttg gct	576
Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala	
180 185 190	
gat tac acc gtg atg gcc aac gtg ctc ggt gcc gac acc gac cca gag	624
Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu	
195 200 205	
atg ccc atg gca acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat	672
Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp	
210 215 220	
gcc aag att cac ctc tac ggc aag gga cat cgc ccg gga cga aag att	720
Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile	
225 230 235 240	
ggc cac gtc aac atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa	768
Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu	
245 250 255	
gcc ctg gcc tgc gca tac ttc ctt gtc aac gct cgc tgg gat	810

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp  
 260 265 270

taggtctttt ctgagcgcta gca

833

<210> 932

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 932

Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu Ala  
 1 5 10 15

Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly  
 20 25 30

Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val  
 35 40 45

Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val  
 50 55 60

Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly  
 65 70 75 80

Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val  
 85 90 95

Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln  
 100 105 110

Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val  
 115 120 125

Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly  
 130 135 140

Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr  
 145 150 155 160

Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His  
 165 170 175

Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala  
 180 185 190

Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu  
 195 200 205

Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp  
 210 215 220

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile  
 225 230 235 240

Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu  
 245 250 255

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp

260

265

270

&lt;210&gt; 933

&lt;211&gt; 618

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(595)

&lt;223&gt; RXN02350

&lt;400&gt; 933

aagcatttct ccaacacttt tgatggacag attaacgctt aaaaggcctg ttatagactg 60

ataaaccgat acgtactttt cgcgcttaag gagaatttca gtg ggt cct cta gtt 115  
 Val Gly Pro Leu Val  
 1 5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct 163  
 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala  
 10 15 20

gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211  
 Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val  
 25 30 35

tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca 259  
 Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala  
 40 45 50

cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca 307  
 His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala  
 55 60 65

cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt 355  
 His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly  
 70 75 80 85

gtt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc 403  
 Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser  
 90 95 100

atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt 451  
 Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly  
 105 110 115

ggc gcg aag aat gca ggc cta ctt gcc gtt cgt att ctc ggt gct ggt 499  
 Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly  
 120 125 130

gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg 547  
 Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala  
 135 140 145

aag gaa gtt gaa gcc aag gac gaa gca ctg aag aag cgc ttg ctc ggc 595  
 Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly  
 150 155 160 165

taatgaatcc gatcgtggtg ctg 618

<210> 934  
<211> 165  
<212> PRT  
<213> *Corynebacterium glutamicum*

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<400> 934
Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp
 1             5             10             15
Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe
      20             25             30
Glu Val Gly Val Val Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn
      35             40             45
Tyr Ala Lys Thr Ala His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys
      50             55             60
Ala Gly Gly Ala Ala His Leu Pro Gly Met Val Ala Ala Ala Thr Pro
      65             70             75             80
Leu Pro Val Ile Gly Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu
      85             90             95
Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val Ala
      100            105            110
Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg
      115            120            125
Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp.Tyr
      130            135            140
Gln Glu Asn Met Ala Lys Glu Val Glu Ala Lys Asp Glu Ala Leu Lys
      145            150            155            160
Lys Arg Leu Leu Gly
      165

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<210> 935
<211> 223
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(223)  
<223> FRXA02346
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<400> 935
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ataaaccgat acgtaacttt cgcgcttaag gagaatttca gtg ggt cct cta gtt      115
                                           Val Gly Pro Leu Val
                                           1                               5

ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct      163
Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala

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	10	15	20	
gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc				211
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val				
	25	30	35	
tct gca cac cgc				223
Ser Ala His Arg				
	40			

<210> 936  
 <211> 41  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 936  
 Val Gly Pro Leu Val Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp  
 1 5 10 15  
 Thr Val Ala Pro Ala Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe  
 20 25 30  
 Glu Val Gly Val Val Ser Ala His Arg  
 35 40

<210> 937  
 <211> 252  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (20)..(229)  
 <223> FRXA02350

<400> 937  
 atactaggat ctgcacggtttg gat tcc ttg ctg tcc atc gtc cag atg cca 52  
 Leu Asp Ser Leu Leu Ser Ile Val Gln Met Pro  
 1 5 10  
 ggc ggc gtt cca gtc gcc act gtc tcc atc ggt ggc gcg aag aat gca 100  
 Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala  
 15 20 25  
 ggc cta ctt gcc gtt cgt att ctc ggt gct ggt gat cct tct ttg gtc 148  
 Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val  
 30 35 40  
 acg aag atg gcc gat tac caa gag aat atg gcg aag gaa gtt gaa gcc 196  
 Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala  
 45 50 55  
 aag gac gaa gca ctg aag aag cgc ttg ctc ggc taatgaatcc gatcgtggtg 249  
 Lys Asp Glu Ala Leu Lys Lys Arg Leu Leu Gly  
 60 65 70  
 ctg 252





90	95	100	
gcg tac tgt gag aaa ttc tat gac cgc aac ttc gca tgc acc cgc gat			451
Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe Ala Cys Thr Arg Asp			
105	110	115	
gcc ggg cac act act ttg ttt acc cgt gca aca aaa gag cag gca gag			499
Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr Lys Glu Gln Ala Glu			
120	125	130	
gcc atc atc gac acc ctt gat gat gtt ttc tac gat gcg gat gcg ggt			547
Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr Asp Ala Asp Ala Gly			
135	140	145	
ttc ctg gca tac cca gca act ccc cca gag gct tgc gga gta agc gtg			595
Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala Ser Gly Val Ser Val			
150	155	160	165
ttg gtt gtc gcg gct ggt acc tct gat ctc ccc caa gca aag gaa gca			643
Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro Gln Ala Lys Glu Ala			
170	175	180	
cta cac act gcc tcc tac ttg ggg cgc tcc acc tca ctg att gtt gat			691
Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr Ser Leu Ile Val Asp			
185	190	195	
ttt gga gtg gct ggc atc cac cgc ctg ctt tca tac gaa gaa gaa ctc			739
Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser Tyr Glu Glu Glu Leu			
200	205	210	
cgc gct gcg ggc gtg ctc atc gtt gcc gct gga atg gat ggt gcg cta			787
Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly Met Asp Gly Ala Leu			
215	220	225	
ccc gga gtt gtc gca ggc tta gtg tcc gca cct gtc gtc gca ctg cca			835
Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro Val Val Ala Leu Pro			
230	235	240	245
acc tcc gtg gga tac ggc gca ggt gct gga gga atc gca cca ctt ctg			883
Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly Ile Ala Pro Leu Leu			
250	255	260	
acc atg ctt aac gcc tgc gcg ccg gga gtt gga gtg gtc aac att gat			931
Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly Val Val Asn Ile Asp			
265	270	275	
aac ggc tat gga gca gga cac ctg gct gcg cag att gcg gcg agg			976
Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln Ile Ala Ala Arg			
280	285	290	
taagggtttc gcaggagacg aac			999

&lt;210&gt; 940

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 940

Met	Gln	Thr	Leu	Ala	Ala	Ile	Val	Arg	Ala	Thr	Lys	Gln	Pro	Phe	Glu
1				5				10						15	

Ile Thr Thr Ile Asp Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile  
                   20                                  25                                  30  
 Arg Val Ile Ala Ala Gly Val Arg His Thr Asp Ala Ile Val Arg Asp  
                   35                                  40                                  45  
 Gln Ile Tyr Pro Thr Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala  
                   50                                  55                                  60  
 Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp  
                   65                                  70                                  75                                  80  
 Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys  
                                   85                                  90                                  95  
 Leu Gly Gly Lys Pro Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe  
                   100                                  105                                  110  
 Ala Cys Thr Arg Asp Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr  
                   115                                  120                                  125  
 Lys Glu Gln Ala Glu Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr  
                   130                                  135                                  140  
 Asp Ala Asp Ala Gly Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala  
                   145                                  150                                  155                                  160  
 Ser Gly Val Ser Val Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro  
                                   165                                  170                                  175  
 Gln Ala Lys Glu Ala Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr  
                   180                                  185                                  190  
 Ser Leu Ile Val Asp Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser  
                   195                                  200                                  205  
 Tyr Glu Glu Glu Leu Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly  
                   210                                  215                                  220  
 Met Asp Gly Ala Leu Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro  
                   225                                  230                                  235                                  240  
 Val Val Ala Leu Pro Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly  
                                   245                                  250                                  255  
 Ile Ala Pro Leu Leu Thr Met Leu Asn Ala Cys Ala Pro Gly Val Gly  
                   260                                  265                                  270  
 Val Val Asn Ile Asp Asn Gly Tyr Gly Ala Gly His Leu Ala Ala Gln  
                   275                                  280                                  285  
 Ile Ala Ala Arg  
                   290

&lt;210&gt; 941

&lt;211&gt; 1551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; RXA00619

&lt;400&gt; 941

tcaaaggaag acaccattga aggtgtgctgc aaaatcggag aattcatcaa aaaatagcag 60

cgactagggtt agtttcgggtt cgtggggaat aataatttgc gtg gct gat aaa aag 115  
 Val Ala Asp Lys Lys  
 1 5

aag atc gca aac gtc ctg tgc aac cgt tac gcc tcc gcg gaa ctt tct 163  
 Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser  
 10 15 20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211  
 Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp  
 25 30 35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259  
 Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala  
 40 45 50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307  
 Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala  
 55 60 65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355  
 Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg  
 70 75 80 85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403  
 Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly  
 90 95 100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451  
 Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His  
 105 110 115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499  
 Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala  
 120 125 130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547  
 Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg  
 135 140 145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595  
 Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala  
 150 155 160 165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643  
 Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu  
 170 175 180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691  
 Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala  
 185 190 195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

Gln Asp Met Leu Asp Leu Met	Glu Gly Asp Glu Ala Arg Leu Ser Asp	
200	205	210
ctg gaa acc cgc atc gca gca cac ctc ggc ttt gat cgc gtc ttc gac		787
Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe Asp Arg Val Phe Asp		
215	220	225
tcc gtc ggc cag gtc tac cca cgt tcc ctt gac ttc gat gca gta tct		835
Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp Phe Asp Ala Val Ser		
230	235	240
gct ctg gtt cag ctt ggc tcc ggc cca tca tcg ctg tcc cac acc att		883
Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser Leu Ser His Thr Ile		
	250	255
cgt ctc atg gcc ggc acc gaa act gtt acc gaa ggt ttt aag gaa ggc		931
Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu Gly Phe Lys Glu Gly		
	265	270
cag gtc ggt tcc tct gca atg cct cac aag atg aac gct cgc tcc tgt		979
Gln Val Gly Ser Ser Ala Met Pro His Lys Met Asn Ala Arg Ser Cys		
	280	285
gag cgc gtg ggc ggc ctg cag gtt att ctt cgc gga tac ctc acc atg		
1027		
Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg Gly Tyr Leu Thr Met		
	295	300
ggt gct gat ctt tcc ggc cag cag tgg aac gaa ggc gat gtc ttc tgc		
1075		
Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu Gly Asp Val Phe Cys		
310	315	320
tcc gtg atc cgc cgc gtt gca ctg cca gac gca ttc ttc gcg att gac		
1123		
Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala Phe Phe Ala Ile Asp		
	330	335
gga atg ttt gaa act ttc ctg aca gtc ctg gat gaa ttc ggt gca ttc		
1171		
Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp Glu Phe Gly Ala Phe		
	345	350
cct gcc atg atc gag cgc gaa ctt gag cgt tac ctg cca ttc ctg gca		
1219		
Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr Leu Pro Phe Leu Ala		
	360	365
act acc cgt atc ctc atg gcc gct gtc cgc gca ggc gtt ggc cgc gaa		
1267		
Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala Gly Val Gly Arg Glu		
	375	380
acc gca cac gaa gta atc aag gaa aac gct gtc gcg gtt gcc ctc aac		
1315		
Thr Ala His Glu Val Ile Lys Glu Asn Ala Val Ala Val Ala Leu Asn		
390	395	400
atg cgc gaa aat ggc ggt gac cag gac ctt atc cag cgc ctc gct gct		
1363		
Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile Gln Arg Leu Ala Ala		

410 415 420  
 gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct  
 1411  
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala  
 425 430 435  
 gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg  
 1459  
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val  
 440 445 450  
 ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac  
 1507  
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp  
 455 460 465  
 tac cga cca ggt gag att ctt taaaggtttt taacggcggtt cac  
 1551  
 Tyr Arg Pro Gly Glu Ile Leu  
 470 475

<210> 942  
 <211> 476  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 942  
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 20 25 30  
 Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly  
 35 40 45  
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp  
 50 55 60  
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His  
 65 70 75 80  
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu  
 85 90 95  
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu  
 100 105 110  
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile  
 115 120 125  
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu  
 130 135 140  
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu  
 145 150 155 160  
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu  
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly  
 180 185 190  
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu  
 195 200 205  
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe  
 210 215 220  
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp  
 225 230 235 240  
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser  
 245 250 255  
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu  
 260 265 270  
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met  
 275 280 285  
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg  
 290 295 300  
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu  
 305 310 315 320  
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala  
 325 330 335  
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp  
 340 345 350  
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr  
 355 360 365  
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala  
 370 375 380  
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val  
 385 390 395 400  
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile  
 405 410 415  
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu  
 420 425 430  
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser  
 435 440 445  
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His  
 450 455 460  
 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu  
 465 470 475

&lt;210&gt; 943

&lt;211&gt; 1683

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1660)

&lt;223&gt; RXA02622

&lt;400&gt; 943

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caggggtggcg tacaactcaa ctggagaggc taaatccttc atg agc gat gat cgt 115
                                         Met Ser Asp Asp Arg
                                         1 5
aag gca att aaa cgc gca cta att agc gtg tat gac aag act ggc ctg 163
Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr Asp Lys Thr Gly Leu
                        10 15 20
gag gat cta gcc cag gca ctt cac cgc gag aac gtg gaa att gtt tcc 211
Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn Val Glu Ile Val Ser
                        25 30 35
acc gga tcc act gcg gcg aag att gct gag ctt ggt att cct gtt acc 259
Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu Gly Ile Pro Val Thr
                        40 45 50
ccg gtt gag gag ctc acc ggt ttc cct gag tgc ctt gag ggc cgt gtg 307
Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys Leu Glu Gly Arg Val
                        55 60 65
aag aca ctg cac cct aag gtt cac gct ggc atc ttg gcg gac acc cgc 355
Lys Thr Leu His Pro Lys Val His Ala Gly Ile Leu Ala Asp Thr Arg
                        70 75 80 85
aag gaa gac cac ctg cgt cag ctc aag gaa ctt gag gtc gcc cca ttc 403
Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu Glu Val Ala Pro Phe
                        90 95 100
cag ctt gtc gtg gtg aac ctg tac cca ttt gct gag acc gtt gcg tcc 451
Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala Glu Thr Val Ala Ser
                        105 110 115
ggc gcc gat ttc gat gct tgc gtt gag cag atc gac atc gga ggc cca 499
Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile Asp Ile Gly Gly Pro
                        120 125 130
tcc atg gtt cgt gct gcg gca aag aac cac cca tct gtc gct gtg gtt 547
Ser Met Val Arg Ala Ala Ala Lys Asn His Pro Ser Val Ala Val Val
                        135 140 145
gtt tca ccg aac cgc tac gag gat gtc cag gaa gct ttg aag acc ggt 595
Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu Ala Leu Lys Thr Gly
                        150 155 160 165
gga ttc tcc cgc gcg gag cgc acc aag ttg gct gct gag gct ttc cgc 643
Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala Ala Glu Ala Phe Arg
                        170 175 180
cac acc gca acc tac gat gtc acc gtt gca acc tgg atg agc gag cag 691
His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr Trp Met Ser Glu Gln

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185	190	195	
ctg gct gcc gaa gat tct gag act gag ttc cca ggt tgg atc ggc acc Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro Gly Trp Ile Gly Thr 200 205 210			739
acc aac acc ttg tcc cgc agc ttg cgt tac ggt gag aac cct cac cag Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly Glu Asn Pro His Gln 215 220 225			787
tct gca gct ttg tac gtg ggc aac acc cgc gga ctt gca cag gct aag Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly Leu Ala Gln Ala Lys 230 235 240 245			835
cag ttc cac ggc aag gaa atg agc tac aac aac tac acc gat tct gat Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn Tyr Thr Asp Ser Asp 250 255 260			883
gct gca tgg cgt gca gcg tgg gat cac gag cgt cct tgt gta gct atc Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg Pro Cys Val Ala Ile 265 270 275			931
atc aag cat gca aac cct tgt ggc att gct gtt tct gat gag tcc atc Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val Ser Asp Glu Ser Ile 280 285 290			979
gca gcg gca cac cgc gag gca cac gca tgt gac tct gtg tcc gca ttc 1027 Ala Ala Ala His Arg Glu Ala His Ala Cys Asp Ser Val Ser Ala Phe 295 300 305			
ggt ggc gtc atc gcg tcc aac cgt gaa gtc agc gtt gag atg gct aac 1075 Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser Val Glu Met Ala Asn 310 315 320 325			
cag gtt gca gag atc ttc act gag gtc atc atc gct cct tcc tat gaa 1123 Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile Ala Pro Ser Tyr Glu 330 335 340			
gag ggc gct gtg gag atc ctg agc cag aag aag aac atc cgt att ctt 1171 Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys Asn Ile Arg Ile Leu 345 350 355			
cag gct gaa gca cct gtg cgt aag ggc ttt gag tcc cgt gag atc tcc 1219 Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu Ser Arg Glu Ile Ser 360 365 370			
ggc ggt ctg ctt gtt cag gaa cgc gac ttg atc cac gct gag ggc gac 1267 Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile His Ala Glu Gly Asp 375 380 385			
aac tcc gca aac tgg act ctt gct gcc ggc tct gct gtt tct cct gag 1315 Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser Ala Val Ser Pro Glu 390 395 400 405			



gtt ctg aag gac ctg gag ttc gcg tgg act gca gtt cgt tcc gtg aag  
 1363  
 Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys  
                   410                  415                  420

tcc aac gca att ctg ttg gct aag aac ggc gct acc gtt ggc gtt ggc  
 1411  
 Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala Thr Val Gly Val Gly  
                   425                  430                  435

atg gga cag gtc aac cgc gtt gac tct gct cgc ttg gct gtc gac cgt  
 1459  
 Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg Leu Ala Val Asp Arg  
                   440                  445                  450

gca ggt gca gag cgc gct acc ggt tcc gtt gct gct tcc gat gcg ttc  
 1507  
 Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala Ala Ser Asp Ala Phe  
                   455                  460                  465

ttc cca ttc gct gat ggc ttt gag gtt ctc gct gag gct ggc atc act  
 1555  
 Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr  
 470                  475                  480                  485

gct gtt gtg cag cct ggt gga tcc att cgc gac aac gag gtc att gag  
 1603  
 Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp Asn Glu Val Ile Glu  
                   490                  495                  500

gca gcc aac aag gct ggc gtg acc atg tac ctg act ggt gcg cga cac  
 1651  
 Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu Thr Gly Ala Arg His  
                   505                  510                  515

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 1683  
 Phe Ala His  
                   520

<210> 944

<211> 520

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 944

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Asp Lys Thr Gly Leu Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn  
                   20                  25                  30

Val Glu Ile Val Ser Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu  
                   35                  40                  45

Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys  
   50                  55                  60

Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile  
   65                  70                  75                  80

Leu Ala Asp Thr Arg Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu  
                                     85                                    90                                    95  
 Glu Val Ala Pro Phe Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala  
                                     100                                    105                                    110  
 Glu Thr Val Ala Ser Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile  
                                     115                                    120                                    125  
 Asp Ile Gly Gly Pro Ser Met Val Arg Ala Ala Ala Lys Asn His Pro  
                                     130                                    135                                    140  
 Ser Val Ala Val Val Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu  
                                     145                                    150                                    155                                    160  
 Ala Leu Lys Thr Gly Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala  
                                     165                                    170                                    175  
 Ala Glu Ala Phe Arg His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr  
                                     180                                    185                                    190  
 Trp Met Ser Glu Gln Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro  
                                     195                                    200                                    205  
 Gly Trp Ile Gly Thr Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly  
                                     210                                    215                                    220  
 Glu Asn Pro His Gln Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly  
                                     225                                    230                                    235                                    240  
 Leu Ala Gln Ala Lys Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn  
                                     245                                    250                                    255  
 Tyr Thr Asp Ser Asp Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg  
                                     260                                    265                                    270  
 Pro Cys Val Ala Ile Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val  
                                     275                                    280                                    285  
 Ser Asp Glu Ser Ile Ala Ala Ala His Arg Glu Ala His Ala Cys Asp  
                                     290                                    295                                    300  
 Ser Val Ser Ala Phe Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser  
                                     305                                    310                                    315                                    320  
 Val Glu Met Ala Asn Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile  
                                     325                                    330                                    335  
 Ala Pro Ser Tyr Glu Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys  
                                     340                                    345                                    350  
 Asn Ile Arg Ile Leu Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu  
                                     355                                    360                                    365  
 Ser Arg Glu Ile Ser Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile  
                                     370                                    375                                    380  
 His Ala Glu Gly Asp Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser  
                                     385                                    390                                    395                                    400

Ala Val Ser Pro Glu Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala  
 405 410 415

Val Arg Ser Val Lys Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala  
 420 425 430

Thr Val Gly Val Gly Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg  
 435 440 445

Leu Ala Val Asp Arg Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala  
 450 455 460

Ala Ser Asp Ala Phe Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala  
 465 470 475 480

Glu Ala Gly Ile Thr Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp  
 485 490 495

Asn Glu Val Ile Glu Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu  
 500 505 510

Thr Gly Ala Arg His Phe Ala His  
 515 520

<210> 945  
 <211> 1641  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1618)  
 <223> RXN00488

<400> 945  
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tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115  
 Met Thr Thr Gln Ser  
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163  
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly  
 10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211  
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val  
 25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259  
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu  
 40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307  
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg  
 55 60 65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355  
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg  
 70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt	403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg	
90 95 100	
tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg	451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met	
105 110 115	
agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt	499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly	
120 125 130	
ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac	547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn	
135 140 145	
cgc gat atg cgt ttt gaa agc gac atg aac cgt cgt gtc gct gaa gtt	595
Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val	
150 155 160 165	
atg acc cca atg cct ttg gtt gtt gct gaa gag ggc gtc acc aag gag	643
Met Thr Pro Met Pro Leu Val Val Ala Glu Glu Gly Val Thr Lys Glu	
170 175 180	
cag gct ctt gct ttg ctg tct gca aac aag gtg gag aag ctt cct atc	691
Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
185 190 195	
atc gca aag gac ggc aag ctt gtc ggt ctg atc acg gtg aag gac ttc	739
Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile Thr Val Lys Asp Phe	
200 205 210	
gtt aag act gag cag cac ccg aac gca tcc aag gat gca tca ggt cgt	787
Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys Asp Ala Ser Gly Arg	
215 220 225	
ctg ctg gtt gcg gct ggc atc ggc acg ggc gag gag tca ttc cag cga	835
Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu Glu Ser Phe Gln Arg	
230 235 240 245	
gct ggt gcg ctt gcc gac gcc ggc gtc gac att ttg gtc gta gac tct	883
Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile Leu Val Val Asp Ser	
250 255 260	
gca cac gcc cat agc cgt gga gtt ttg gac atg gtg tcc cgc gtg aag	931
Ala His Ala His Ser Arg Gly Val Leu Asp Met Val Ser Arg Val Lys	
265 270 275	
aag tcg ttc ccc aag gtc gat atc gtt ggc ggc aac ttg gcg acc cgc	979
Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly Asn Leu Ala Thr Arg	
280 285 290	
gag gct gcg cag gcc atg att gaa gct ggc gca gac gct atc aag gtg	1027
Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala Asp Ala Ile Lys Val	
295 300 305	
ggg att ggc cca ggt tct att tgc acc act cgc gtt gtc gca ggt gtc	1075
Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val	

310	315	320	325
ggt gca cct cag atc act gcg atc atg gag gca gct gtt cca gct cac			
1123			
Gly Ala Pro Gln	Ile Thr Ala Ile	Met Glu Ala Ala	Val Pro Ala His
	330	335	340
aag gct ggc gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt			
1171			
Lys Ala Gly Val	Pro Ile Ile Ala	Asp Gly Gly Met	Gln Phe Ser Gly
	345	350	355
gat atc gct aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc			
1219			
Asp Ile Ala Lys	Ala Leu Ala Ala	Gly Ala Asn Ser	Val Met Leu Gly
	360	365	370
tcc atg ctg gct ggt acc gct gag gct cct ggt gag acc atc acc atc			
1267			
Ser Met Leu Ala	Gly Thr Ala Glu	Ala Pro Gly Glu	Thr Ile Thr Ile
	375	380	385
aac ggc aag cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct			
1315			
Asn Gly Lys Gln	Tyr Lys Arg Tyr	Arg Gly Met Gly	Ser Met Gly Ala
	395	400	405
atg cag ggc cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac			
1363			
Met Gln Gly Arg	Gly Leu Ser Gly	Glu Lys Arg Ser	Tyr Ser Lys Asp
	410	415	420
cgt tac ttc cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa			
1411			
Arg Tyr Phe Gln	Ser Asp Val Lys	Ser Glu Asp Lys	Leu Val Pro Glu
	425	430	435
ggc atc gaa ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att			
1459			
Gly Ile Glu Gly	Arg Val Pro Phe	Arg Gly Pro Ile	Gly Asp Ile Ile
	440	445	450
cac cag cag gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc			
1507			
His Gln Gln Val	Gly Gly Leu Arg	Ala Ala Met Gly	Tyr Thr Gly Ser
	455	460	465
tcc acc att gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc			
1555			
Ser Thr Ile Glu	Glu Leu His Asn	Ala Arg Phe Val	Gln Ile Thr Ser
	475	480	485
gcg ggt ctg aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa			
1603			
Ala Gly Leu Lys	Glu Ser His Pro	His His Ile Gln	Gln Thr Val Glu
	490	495	500
gct cct aac tac cac tagattttgc tcacttaaagc agc			
1641			
Ala Pro Asn Tyr	His		
	505		

&lt;210&gt; 946

&lt;211&gt; 506

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 946

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Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
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Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
      20              25              30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
      35              40              45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
      50              55              60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
      65              70              75              80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
      85              90              95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
      100             105             110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
      115             120             125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
      130             135             140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg
      145             150             155             160

Arg Val Ala Glu Val Met Thr Pro Met Pro Leu Val Val Ala Glu Glu
      165             170             175

Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val
      180             185             190

Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile
      195             200             205

Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys
      210             215             220

Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu
      225             230             235             240

Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile
      245             250             255

Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met
      260             265             270

Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly
      275             280             285

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Asn Leu Ala Thr Arg Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala  
 290 295 300  
 Asp Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg  
 305 310 315 320  
 Val Val Ala Gly Val Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala  
 325 330 335  
 Ala Val Pro Ala His Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly  
 340 345 350  
 Met Gln Phe Ser Gly Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn  
 355 360 365  
 Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly  
 370 375 380  
 Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met  
 385 390 395 400  
 Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg  
 405 410 415  
 Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp  
 420 425 430  
 Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro  
 435 440 445  
 Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met  
 450 455 460  
 Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe  
 465 470 475 480  
 Val Gln Ile Thr Ser Ala Gly Leu Lys Glu Ser His Pro His His Ile  
 485 490 495  
 Gln Gln Thr Val Glu Ala Pro Asn Tyr His  
 500 505  
  
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 <213> Corynebacterium glutamicum  
  
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 <223> FRXA00492  
  
 <400> 947  
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 tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115  
 Met Thr Thr Gln Ser  
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163  
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly  
 10 15 20  
 tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211  
 Leu Thr Phe Asp Asp Val Leu Leu Pro Asp Ala Ser Asp Val Val  
 25 30 35  
 cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259  
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu  
 40 45 50  
 aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307  
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg  
 55 60 65  
 atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355  
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg  
 70 75 80 85  
 aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403  
 Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg  
 90 95 100  
 tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451  
 Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met  
 105 110 115  
 agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499  
 Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly  
 120 125 130  
 ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547  
 Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn  
 135 140 145  
 cgc gat atg cgt ttt gaa agc gac atg 574  
 Arg Asp Met Arg Phe Glu Ser Asp Met  
 150 155

&lt;210&gt; 948

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 948

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys  
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 Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp  
 20 25 30  
 Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr  
 35 40 45  
 Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr  
 50 55 60  
 Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile  
 65 70 75 80



Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val  
85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr  
100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg  
115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val  
130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met  
145 150 155

<210> 949

<211> 557

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(534)

<223> FRXA00488

<400> 949

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gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt gat atc gct 96  
Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala  
20 25 30

aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc tcc atg ctg 144  
Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu  
35 40 45

gct ggt acc gct gag gct cct ggt gag acc atc acc atc aac ggc aag 192  
Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys  
50 55 60

cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct atg cag ggc 240  
Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly  
65 70 75 80

cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac cgt tac ttc 288  
Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe  
85 90 95

cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa ggc atc gaa 336  
Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu  
100 105 110

ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att cac cag cag 384  
Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln  
115 120 125

gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc tcc acc att 432

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile  
 130 135 140

gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc gcg ggt ctg 480  
 Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu  
 145 150 155 160

aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa gct cct aac 528  
 Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn  
 165 170 175

tac cac tagattttgc tcacttaaagc agc 557  
 Tyr His

<210> 950  
 <211> 178  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 950  
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Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala  
 20 25 30

Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu  
 35 40 45

Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys  
 50 55 60

Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly  
 65 70 75 80

Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe  
 85 90 95

Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu  
 100 105 110

Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln  
 115 120 125

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile  
 130 135 140

Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu  
 145 150 155 160

Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn  
 165 170 175

Tyr His

<210> 951  
 <211> 1554

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1531)

&lt;223&gt; RXA02469

&lt;400&gt; 951

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gccgtgttca gggataactg attaatacaac taggagaccc atg cgt ttt ctt aac 115  
 Met Arg Phe Leu Asn  
 1 5

aat tcc aat ccg ccc tat gag ctg aca tat tcc gat gtg ttt atg gtg 163  
 Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser Asp Val Phe Met Val  
 10 15 20

cct tcg cgt tct gac gta ggc tcc cgc atg tcc gtg gat ctg cgc acc 211  
 Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser Val Asp Leu Arg Thr  
 25 30 35

aat gac gga act gga aca acc atc ccg ctc gtt gtg gca aac atg act 259  
 Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val Val Ala Asn Met Thr  
 40 45 50

gct gtt gct ggc cga cgc atg gct gag acc att gcg cgc cgc ggt ggc 307  
 Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile Ala Arg Arg Gly Gly  
 55 60 65

atg gcg att ctt ccg cag gat gtg ccc gcc gat att gct gca gag act 355  
 Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp Ile Ala Ala Glu Thr  
 70 75 80 85

atc gcg aat gtg aag aaa gcg gac ctg gtt ttt gat acc cca att acc 403  
 Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr  
 90 95 100

gta aaa ccg cac cac acc gtg ggt tat gca cgc aac ttg atc cac aag 451  
 Val Lys Pro His His Thr Val Gly Tyr Ala Arg Asn Leu Ile His Lys  
 105 110 115

cgt gcg cac ggt gca gcc att gtt ttg gag ggc gat cag ccg gtc ggc 499  
 Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly Asp Gln Pro Val Gly  
 120 125 130

atc gtc acc gac aag gac ctc gaa ggc gca gac aac ttc act cag gtg 547  
 Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val  
 135 140 145

ggc acc ctc atg tcc acc tcc cta ttg acg ctg cct gag gat att tcc 595  
 Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu Pro Glu Asp Ile Ser  
 150 155 160 165

ccc gaa gac gcc ttc gga atc ctc cac gaa cac agc cgc aaa ctc gcc 643  
 Pro Glu Asp Ala Phe Gly Ile Leu His Glu His Ser Arg Lys Leu Ala  
 170 175 180

ccc gtc gtc gcg gct gac ggc tca ctc cgc ggc atc ctc acc cgc acc 691  
 Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly Ile Leu Thr Arg Thr

185					190					195					
ggc gcc ctg cgc gcc acc atg tac aag ccg gct atc gac gcc aac ggc	739														
Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala Ile Asp Ala Asn Gly															
200	205														
cgc ctg cga gtc ggc gcc gcc atc ggc atc aac ggc gac atc gaa gga	787														
Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn Gly Asp Ile Glu Gly															
215	220														
cgc acc aaa acg ctt ctc gac gcc ggc gcc gac gtt cta gtc gtc gac	835														
Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp Val Leu Val Val Asp															
230	235														
aca gca cac ggc cac caa tcc acc atg atc agc gcc ctc aaa cgc atc	883														
Thr Ala His Gly His Gln Ser Thr Met Ile Ser Ala Leu Lys Arg Ile															
250	255														
cgc gca ctc gac gtc aac gtc ccc atc gtt gct ggc aac gtg gtc acc	931														
Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala Gly Asn Val Val Thr															
265	270														
gcc gat ggt gtc cgc gac cta gtt gaa gca ggc gca aac atc atc aag	979														
Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asn Ile Ile Lys															
280	285														
gta ggc gtt gga cca ggc gca atg tgc acc acc cgc atg caa acc ggc	1027														
Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Gln Thr Gly															
295	300														
gtt ggc cga cca cag ttc tcc gca gtg ctg gaa tgc gca gcc gaa gcc	1075														
Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu Cys Ala Ala Glu Ala															
310	315														
cgc aaa ctc ggc gca cac gta tgg gca gac ggc gga gtc cgc gac ccc	1123														
Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly Gly Val Arg Asp Pro															
330	335														
cgc gac gtc gcc ctg gca ctc gca gct ggc gcc tcc aac gtg atg gtc	1171														
Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala Ser Asn Val Met Val															
345	350														
gga tcc tgg ttc tcc gga acc tac gaa tcc ccc ggc gac ctc cgc ttc	1219														
Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro Gly Asp Leu Arg Phe															
360	365														
gaa tcc gac gga cgc atg tac aaa gaa tcc ttc ggt atg gca tcc cgg	1267														
Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe Gly Met Ala Ser Arg															
375	380														
cgc gcc gtg gaa agc cga aac caa aag gtc gaa gct ttc gaa aaa gca	1315														
Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu Ala Phe Glu Lys Ala															
390	395														

cgc cgc gca atg ttc gaa gaa ggc atc tcc act gcc cgc atc tac att  
1363

Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr Ala Arg Ile Tyr Ile  
410 415 420

gac aaa cgc cac ggc gga gtc gag gac ctg gta gat caa atc atc tcc  
1411

Asp Lys Arg His Gly Gly Val Glu Asp Leu Val Asp Gln Ile Ile Ser  
425 430 435

ggc gtc cgc tcc tca ttc acc tac gca ggc gcc gat tcg att gaa acc  
1459

Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala Asp Ser Ile Glu Thr  
440 445 450

ttc ttc gaa cgc gcc acc gtc gga gtt caa tcc acc gaa ggc tac gca  
1507

Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser Thr Glu Gly Tyr Ala  
455 460 465

gaa gga aag cca cgc gct tcg cgt taagtgttg tgtgcctttg aga  
1554

Glu Gly Lys Pro Arg Ala Ser Arg  
470 475

<210> 952

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 952

Met Arg Phe Leu Asn Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser  
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Asp Val Phe Met Val Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser  
20 25 30

Val Asp Leu Arg Thr Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val  
35 40 45

Val Ala Asn Met Thr Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile  
50 55 60

Ala Arg Arg Gly Gly Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp  
65 70 75 80

Ile Ala Ala Glu Thr Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe  
85 90 95

Asp Thr Pro Ile Thr Val Lys Pro His His Thr Val Gly Tyr Ala Arg  
100 105 110

Asn Leu Ile His Lys Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly  
115 120 125

Asp Gln Pro Val Gly Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp  
130 135 140

Asn Phe Thr Gln Val Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu  
145 150 155 160

Pro Glu Asp Ile Ser Pro Glu Asp Ala Phe Gly Ile Leu His Glu His  
 165 170 175  
 Ser Arg Lys Leu Ala Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly  
 180 185 190  
 Ile Leu Thr Arg Thr Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala  
 195 200 205  
 Ile Asp Ala Asn Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn  
 210 215 220  
 Gly Asp Ile Glu Gly Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp  
 225 230 235 240  
 Val Leu Val Val Asp Thr Ala His Gly His Gln Ser Thr Met Ile Ser  
 245 250 255  
 Ala Leu Lys Arg Ile Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala  
 260 265 270  
 Gly Asn Val Val Thr Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly  
 275 280 285  
 Ala Asn Ile Ile Lys Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr  
 290 295 300  
 Arg Met Gln Thr Gly Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu  
 305 310 315 320  
 Cys Ala Ala Glu Ala Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly  
 325 330 335  
 Gly Val Arg Asp Pro Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala  
 340 345 350  
 Ser Asn Val Met Val Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro  
 355 360 365  
 Gly Asp Leu Arg Phe Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe  
 370 375 380  
 Gly Met Ala Ser Arg Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu  
 385 390 395 400  
 Ala Phe Glu Lys Ala Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr  
 405 410 415  
 Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val  
 420 425 430  
 Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala  
 435 440 445  
 Asp Ser Ile Glu Thr Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser  
 450 455 460  
 Thr Glu Gly Tyr Ala Glu Gly Lys Pro Arg Ala Ser Arg  
 465 470 475

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<210> 953
<211> 1692
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1669)
<223> RXN00487
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<400> 953																
agggcgccag gggcatccag ccattaaagc ttttcgacga gccctcgccc atgtggccaa																60
agaatcttat ttggaggctc gtctagtaga gtgagttctt																
										gtg	agc	ctt	cag	aca		115
										Val	Ser	Leu	Gln	Thr		
										1				5		
aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag																163
Asn	His	Arg	Pro	Val	Leu	Val	Val	Asp	Phe	Gly	Ala	Gln	Tyr	Ala	Gln	
				10					15					20		
ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc																211
Leu	Ile	Ala	Arg	Arg	Val	Arg	Glu	Ala	Gly	Ile	Tyr	Ser	Glu	Val	Ile	
			25					30					35			
ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc																259
Pro	His	Thr	Ala	Thr	Ala	Asp	Asp	Val	Arg	Ala	Lys	Asn	Ala	Ala	Ala	
		40					45					50				
ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca																307
Leu	Val	Leu	Ser	Gly	Gly	Pro	Ser	Ser	Val	Tyr	Ala	Glu	Gly	Ala	Pro	
	55					60					65					
tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att																355
Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu	Pro	Val	Phe	Gly	Ile	
70					75					80				85		
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc																403
Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu	Gly	Gly	Thr	Val	Ala	
				90					95					100		
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt																451
Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp	Ile	Asn	Val	Ala	Gly	
			105					110					115			
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc																499
Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His	Lys	Val	Trp	Met	Ser	
		120				125						130				
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg																547
His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly	Phe	Val	Val	Thr	Ala	
	135					140					145					
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa																595
Ser	Ser	Glu	Gly	Ala	Pro	Val	Ala	Ala	Phe	Glu	Asn	Lys	Glu	Arg	Lys	
150					155					160				165		
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc																643
Met	Ala	Gly	Val	Gln	Tyr	His	Pro	Glu	Val	Leu	His	Ser	Pro	His	Gly	
				170				175						180		

cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag 691  
 Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln  
 185 190 195

aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc 739  
 Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg  
 200 205 210

gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt 787  
 Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly  
 215 220 225

gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac 835  
 Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp  
 230 235 240 245

cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag 883  
 Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu  
 250 255 260

cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg 931  
 Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu  
 265 270 275

gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt 979  
 Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val  
 280 285 290

acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc  
 1027  
 Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg  
 295 300 305

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt  
 1075  
 Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly  
 310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg  
 1123  
 Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val  
 330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac  
 1171  
 Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn  
 345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg  
 1219  
 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu  
 360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc  
 1267  
 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly  
 375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt  
 1315



Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu  
 390 395 400 405

ggc atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc  
 1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu  
 410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt  
 1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu  
 425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc  
 1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg  
 440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc acc tac gga cac cca atc gtg  
 1507

Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr Gly His Pro Ile Val  
 455 460 465

ctg cgc cca gtg tct tcc gaa gac gca atg acc gcc gac tgg acc cgc  
 1555

Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr Ala Asp Trp Thr Arg  
 470 475 480 485

ctg cca tac gag gtt ctg gag aag atc tcc acc cgc atc acc aac gaa  
 1603

Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr Arg Ile Thr Asn Glu  
 490 495 500

gtt cca gat gtg aac cgc gtg gtg ctg gac gta acc tcc aag cca cca  
 1651

Val Pro Asp Val Asn Arg Val Val Leu Asp Val Thr Ser Lys Pro Pro  
 505 510 515

gga acc atc gaa tgg gag taggccttaa atgagccttc gtt  
 1692

Gly Thr Ile Glu Trp Glu  
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<210> 954

<211> 523

<212> PRT

<213> Corynebacterium glutamicum

<400> 954

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly  
 1 5 10 15

Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile  
 20 25 30

Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala  
 35 40 45

Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr  
 50 55 60

Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu  
 65 70 75 80  
 Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu  
 85 90 95  
 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp  
 100 105 110  
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His  
 115 120 125  
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly  
 130 135 140  
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu  
 145 150 155 160  
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu  
 165 170 175  
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile  
 180 185 190  
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu  
 195 200 205  
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys  
 210 215 220  
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln  
 225 230 235 240  
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu  
 245 250 255  
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala  
 260 265 270  
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser  
 275 280 285  
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly  
 290 295 300  
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu  
 305 310 315 320  
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu  
 325 330 335  
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile  
 340 345 350  
 Lys Ser His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys  
 355 360 365  
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val  
 370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe  
385 390 395 400

Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp  
405 410 415

Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu  
420 425 430

Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu  
435 440 445

Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr  
450 455 460

Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr  
465 470 475 480

Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr  
485 490 495

Arg Ile Thr Asn Glu Val Pro Asp Val Asn Arg Val Val Leu Asp Val  
500 505 510

Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu  
515 520

<210> 955

<211> 1486

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1486)

<223> FRXA00487

<400> 955

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agaatcttat ttggaggctc gtctagtaga gtgagttctt gtg agc ctt cag aca 115  
Val Ser Leu Gln Thr  
1 5

aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163  
Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln  
10 15 20

ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211  
Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile  
25 30 35

ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259  
Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala  
40 45 50

ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307  
Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro  
55 60 65

tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att	355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile	
70 75 80 85	
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc	403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala	
90 95 100	
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt	451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly	
105 110 115	
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser	
120 125 130	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
135 140 145	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
150 155 160 165	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
170 175 180	
cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	
1027	
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt  
1075

Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly  
310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg  
1123

Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val  
330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac  
1171

Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn  
345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg  
1219

Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu  
360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc  
1267

Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly  
375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt  
1315

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu  
390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc  
1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu  
410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt  
1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu  
425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc  
1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg  
440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc  
1486

Ser Val Gly Val Gln Gly Asp Gly Arg  
455 460

<210> 956

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 956

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly  
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Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile

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Tyr	Ser	Glu	Val	Ile	Pro	His	Thr	Ala	Thr	Ala	Asp	Asp	Val	Arg	Ala
		35					40					45			
Lys	Asn	Ala	Ala	Ala	Leu	Val	Leu	Ser	Gly	Gly	Pro	Ser	Ser	Val	Tyr
	50					55					60				
Ala	Glu	Gly	Ala	Pro	Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu
	65					70					75				80
Pro	Val	Phe	Gly	Ile	Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu
				85					90					95	
Gly	Gly	Thr	Val	Ala	Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp
			100					105					110		
Ile	Asn	Val	Ala	Gly	Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His
		115					120					125			
Lys	Val	Trp	Met	Ser	His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly
	130					135					140				
Phe	Val	Val	Thr	Ala	Ser	Ser	Glu	Gly	Ala	Pro	Val	Ala	Ala	Phe	Glu
	145					150					155				160
Asn	Lys	Glu	Arg	Lys	Met	Ala	Gly	Val	Gln	Tyr	His	Pro	Glu	Val	Leu
				165					170					175	
His	Ser	Pro	His	Gly	Gln	Ala	Val	Leu	Thr	Arg	Phe	Leu	Thr	Glu	Ile
			180					185					190		
Ala	Gly	Leu	Glu	Gln	Asn	Trp	Thr	Ala	Ala	Asn	Ile	Ala	Glu	Glu	Leu
		195					200					205			
Ile	Glu	Lys	Val	Arg	Glu	Gln	Ile	Gly	Glu	Asp	Gly	Arg	Ala	Ile	Cys
	210					215					220				
Gly	Leu	Ser	Gly	Gly	Val	Asp	Ser	Ala	Val	Ala	Gly	Ala	Leu	Val	Gln
	225					230					235				240
Arg	Ala	Ile	Gly	Asp	Arg	Leu	Thr	Cys	Val	Phe	Val	Asp	His	Gly	Leu
				245					250					255	
Leu	Arg	Ala	Gly	Glu	Arg	Glu	Gln	Val	Glu	Lys	Asp	Phe	Val	Ala	Ala
			260					265					270		
Thr	Gly	Ala	Lys	Leu	Val	Thr	Val	Asp	Glu	Arg	Gln	Ala	Phe	Leu	Ser
		275					280					285			
Lys	Leu	Ala	Gly	Val	Thr	Glu	Pro	Glu	Ala	Lys	Arg	Lys	Ala	Ile	Gly
	290					295					300				
Ala	Glu	Phe	Ile	Arg	Ser	Phe	Glu	Arg	Ala	Val	Ala	Gly	Val	Leu	Glu
	305					310					315				320
Glu	Ala	Pro	Glu	Gly	Ser	Thr	Val	Asp	Phe	Leu	Val	Gln	Gly	Thr	Leu
				325					330					335	
Tyr	Pro	Asp	Val	Val	Glu	Ser	Gly	Gly	Gly	Ser	Gly	Thr	Ala	Asn	Ile
			340					345					350		

Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys  
 355 360 365

Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val  
 370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe  
 385 390 395 400

Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp  
 405 410 415

Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu  
 420 425 430

Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu  
 435 440 445

Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg  
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<210> 957

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<223> RXA02237

<400> 957

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gcacttctcg agcgtttcgg cttcgaggat taattcttca gtg tcg ggc gat aac 115  
 Val Ser Gly Asp Asn  
 1 5

caa cta gga cgg ctc gta att ctt gcg ggc ccc tca gcg gtc ggt aaa 163  
 Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro Ser Ala Val Gly Lys  
 10 15 20

tcg act gtg gtt gat cgc ctc cgc aat gac gtt cca aac ctg tat ttc 211  
 Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val Pro Asn Leu Tyr Phe  
 25 30 35

agt gtg tcg atg acc act agg gca cct cgt cct ggt gaa gtc gat gga 259  
 Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro Gly Glu Val Asp Gly  
 40 45 50

cgt gac tac ttc tat gtc act gca cag gaa ttt cag gac aaa atc gac 307  
 Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe Gln Asp Lys Ile Asp  
 55 60 65

tgt gga gag atg ctt gaa tgg gca gat atc cac ggc ggt ttg cag cgt 355  
 Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His Gly Gly Leu Gln Arg  
 70 75 80 85

tca ggc act cca gca ggt ccc gtc aat gag gct cgc caa aat ggt cgg 403

Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala Arg Gln Asn Gly Arg  
                             90                            95                            100  
 cca gta ttg gtt gag gtt gat ctt gca gga gcc cga aac atc gct agc 451  
 Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala Arg Asn Ile Ala Ser  
                             105                            110                            115  
 tta att cca gat gca gaa acc atc ttc ctt gct cca cct tca tgg gaa 499  
 Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala Pro Pro Ser Trp Glu  
                             120                            125                            130  
 gtt ttg gtt gaa cgc ctc act gga cgt ggc acc gaa agc gaa gac gtt 547  
 Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr Glu Ser Glu Asp Val  
                             135                            140                            145  
 att gct cgc agg ctc gag acc gca cgc gaa gaa ttg gct gct cag agc 595  
 Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu Leu Ala Ala Gln Ser  
                             150                            155                            160                            165  
 gaa ttt aag cac gtc att atc aat gat gat gtg gat aca gcc gtc aag 643  
 Glu Phe Lys His Val Ile Ile Asn Asp Asp Val Asp Thr Ala Val Lys  
                             170                            175                            180  
 gct att gag gat gtt ctc ctc ggc gct tagccaaaac atagagcggt 690  
 Ala Ile Glu Asp Val Leu Leu Gly Ala  
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 agg 693  
  
 <210> 958  
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 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 958  
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 Ser Ala Val Gly Lys Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val  
                             20                            25                            30  
 Pro Asn Leu Tyr Phe Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro  
                             35                            40                            45  
 Gly Glu Val Asp Gly Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe  
                             50                            55                            60  
 Gln Asp Lys Ile Asp Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His  
                             65                            70                            75                            80  
 Gly Gly Leu Gln Arg Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala  
                             85                            90                            95  
 Arg Gln Asn Gly Arg Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala  
                             100                            105                            110  
 Arg Asn Ile Ala Ser Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala  
                             115                            120                            125  
 Pro Pro Ser Trp Glu Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr



130	135	140
Glu Ser Glu Asp Val	Ile Ala Arg Arg Leu	Glu Thr Ala Arg Glu Glu
145	150	155 160
Leu Ala Ala Gln Ser Glu Phe Lys His Val	Ile Ile Asn Asp Asp Val	
	165 170	175
Asp Thr Ala Val Lys Ala Ile Glu Asp Val Leu Leu Gly Ala		
	180 185	190

&lt;210&gt; 959

&lt;211&gt; 1413

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1390)

&lt;223&gt; RXA01446

&lt;400&gt; 959

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tgcatactcc aacttcatgg atcggatgtg acgtaaacca atg gct gca atc gtt 115
                                         Met Ala Ala Ile Val
                                         1 5

att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat 163
Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp
                        10 15 20

att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac 211
Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn
                        25 30 35

aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag 259
Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys
                        40 45 50

ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc 307
Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly
                        55 60 65

aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc 355
Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly
                        70 75 80 85

ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac 403
Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn
                        90 95 100

gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa 451
Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu
                        105 110 115

cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc 499
Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly
                        120 125 130

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cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac 547  
 Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp  
 135 140 145

att ttc gac gaa tcc atc ctt cgt caa aaa gtc gaa tcc gcc ctg gat 595  
 Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp  
 150 155 160 165

tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc 643  
 Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val  
 170 175 180

gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc 691  
 Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg  
 185 190 195

ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag 739  
 Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln  
 200 205 210

ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg 787  
 Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val  
 215 220 225

gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt 835  
 Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly  
 230 235 240 245

ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc 883  
 Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser  
 250 255 260

ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc 931  
 Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe  
 265 270 275

cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt 979  
 Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly  
 280 285 290

ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac  
 1027  
 Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr  
 295 300 305

gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac  
 1075  
 Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp  
 310 315 320 325

tac ttc ctg acc aag cta gac gtg ctc acc ggc atc ggt gaa atc cca  
 1123  
 Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro  
 330 335 340

atc tgc gta gct tac gac gtt gat ggt gtt cgc cac gat gaa atg cca  
 1171  
 Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro  
 345 350 355

ctg acc cag tca gag ttc cac cac gca acc cca atc ttt gaa acc atg  
1219

Leu Thr Gln Ser Glu Phe His His Ala Thr Pro Ile Phe Glu Thr Met  
360 365 370

cct gca tgg gac gaa gac atc acc gac tgc aag acc ttc gag gat ctt  
1267

Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys Thr Phe Glu Asp Leu  
375 380 385

cca caa aag gcc cag gac tac gtc cga cgt ctg gaa gaa ctc tct ggt  
1315

Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu Glu Glu Leu Ser Gly  
390 395 400 405

gct cgc ttc tcc tac atc ggt gtt gga cct ggt cgc gat cag acc atc  
1363

Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly Arg Asp Gln Thr Ile  
410 415 420

gtc ctg cat gac gta cta gct gac aac tagtactgat aaacatcagt  
1410

Val Leu His Asp Val Leu Ala Asp Asn  
425 430

gag  
1413

<210> 960

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 960

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20 25 30

Pro Asn Gly Gly Asn Asn Ala Gly His Thr Val Val Val Gly Gly Glu  
35 40 45

Lys Tyr Glu Leu Lys Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala  
50 55 60

Thr Pro Ile Leu Gly Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe  
65 70 75 80

Glu Glu Ile Asp Gly Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu  
85 90 95

Arg Ile Ser Ala Asn Ala His Leu Val Ala Pro Tyr His Gln Val Met  
100 105 110

Asp Arg Val Gln Glu Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr  
115 120 125

Gly Arg Gly Ile Gly Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly  
130 135 140

Ile Arg Val Gln Asp Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val  
 145 150 155 160  
 Glu Ser Ala Leu Asp Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn  
 165 170 175  
 Arg Lys Ala Ile Val Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr  
 180 185 190  
 Ala Asp Arg Leu Arg Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn  
 195 200 205  
 Glu Ala Leu Asp Gln Gly Lys His Val Leu Met Glu Gly Gly Gln Ala  
 210 215 220  
 Thr Met Leu Asp Val Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser  
 225 230 235 240  
 Asn Pro Thr Ala Gly Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr  
 245 250 255  
 Lys Ile Thr Ser Ser Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val  
 260 265 270  
 Gly Ala Gly Pro Phe Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr  
 275 280 285  
 Leu Gln Thr Val Gly Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg  
 290 295 300  
 Arg Cys Gly Trp Tyr Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val  
 305 310 315 320  
 Asn Gly Phe Thr Asp Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly  
 325 330 335  
 Ile Gly Glu Ile Pro Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg  
 340 345 350  
 His Asp Glu Met Pro Leu Thr Gln Ser Glu Phe His His Ala Thr Pro  
 355 360 365  
 Ile Phe Glu Thr Met Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys  
 370 375 380  
 Thr Phe Glu Asp Leu Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu  
 385 390 395 400  
 Glu Glu Leu Ser Gly Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly  
 405 410 415  
 Arg Asp Gln Thr Ile Val Leu His Asp Val Leu Ala Asp Asn  
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&lt;210&gt; 961

&lt;211&gt; 1551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<220>  
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 <222> (101)..(1528)  
 <223> RXA00619

<400> 961

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                                   Val Ala Asp Lys Lys
                                   1           5

aag atc gca aac gtc ctg tgc aac cgt tac gcc tcc gcg gaa ctt tct 163
Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
              10              15              20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
              25              30              35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
              40              45              50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
              55              60              65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
              70              75              80              85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403
Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
              90              95              100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
              105              110              115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
              120              125              130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
              135              140              145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
              150              155              160              165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
              170              175              180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
              185              190              195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739
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Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu Ala Arg Leu Ser Asp	
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ctg gaa acc cgc atc gca gca cac ctc ggc ttt gat cgc gtc ttc gac	787
Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe Asp Arg Val Phe Asp	
215 220 225	
tcc gtc ggc cag gtc tac cca cgt tcc ctt gac ttc gat gca gta tct	835
Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp Phe Asp Ala Val Ser	
230 235 240 245	
gct ctg gtt cag ctt ggc tcc ggc cca tca tcg ctg tcc cac acc att	883
Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser Leu Ser His Thr Ile	
250 255 260	
cgt ctc atg gcc ggc acc gaa act gtt acc gaa ggt ttt aag gaa ggc	931
Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu Gly Phe Lys Glu Gly	
265 270 275	
cag gtc ggt tcc tct gca atg cct cac aag atg aac gct cgc tcc tgt	979
Gln Val Gly Ser Ser Ala Met Pro His Lys Met Asn Ala Arg Ser Cys	
280 285 290	
gag cgc gtg ggc ggc ctg cag gtt att ctt cgc gga tac ctc acc atg	
1027	
Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg Gly Tyr Leu Thr Met	
295 300 305	
gtt gct gat ctt tcc ggc cag cag tgg aac gaa ggc gat gtc ttc tgc	
1075	
Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu Gly Asp Val Phe Cys	
310 315 320 325	
tcc gtg atc cgc cgc gtt gca ctg cca gac gca ttc ttc gcg att gac	
1123	
Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala Phe Phe Ala Ile Asp	
330 335 340	
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1171	
Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp Glu Phe Gly Ala Phe	
345 350 355	
cct gcc atg atc gag cgc gaa ctt gag cgt tac ctg cca ttc ctg gca	
1219	
Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr Leu Pro Phe Leu Ala	
360 365 370	
act acc cgt atc ctc atg gcc gct gtc cgc gca ggc gtt ggc cgc gaa	
1267	
Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala Gly Val Gly Arg Glu	
375 380 385	
acc gca cac gaa gta atc aag gaa aac gct gtc gcg gtt gcc ctc aac	
1315	
Thr Ala His Glu Val Ile Lys Glu Asn Ala Val Ala Val Ala Leu Asn	
390 395 400 405	
atg cgc gaa aat ggc ggt gac cag gac ctt atc cag cgc ctc gct gct	
1363	
Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile Gln Arg Leu Ala Ala	

410	415	420
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1411		
Asp Glu Arg Leu Pro Met Ser Glu	Ala Asp Leu Glu Ala	Ala Leu Ala
425	430	435
gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg		
1459		
Asp Arg His Ala Phe Ile Gly Ala Ala	Glu Ser Gln Val Ser Arg Val	
440	445	450
ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac		
1507		
Leu Asp Arg Ile Gln Val Leu Val Asp Ala His	Pro Gly Ala Ala Asp	
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tac cga cca ggt gag att ctt taaaggtttt taacggcgtt cac		
1551		
Tyr Arg Pro Gly Glu Ile Leu		
470	475	
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Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly		
35	40	45
Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp		
50	55	60
Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His		
65	70	75
Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu		
85	90	95
His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu		
100	105	110
Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile		
115	120	125
Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu		
130	135	140
Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu		
145	150	155
Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu		
165	170	175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly  
 180 185 190  
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu  
 195 200 205  
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe  
 210 215 220  
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp  
 225 230 235 240  
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser  
 245 250 255  
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu  
 260 265 270  
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met  
 275 280 285  
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg  
 290 295 300  
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu  
 305 310 315 320  
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala  
 325 330 335  
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp  
 340 345 350  
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr  
 355 360 365  
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala  
 370 375 380  
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val  
 385 390 395 400  
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile  
 405 410 415  
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu  
 420 425 430  
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser  
 435 440 445  
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His  
 450 455 460  
 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu  
 465 470 475

&lt;210&gt; 963

&lt;211&gt; 666



&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(643)

&lt;223&gt; RXA00688

&lt;400&gt; 963

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gcggaaccgc aatcttgatt cttgtatctg ttgcactgac cacagtgaag cagattgaga 60

gccagctcct gcaaagcaac tacgaaggac ttctaaaata atg cga ctc gta ctc 115
                                         Met Arg Leu Val Leu
                                         1           5

ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
              10              15              20

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
              25              30              35

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
              40              45              50

gac gct ggc aag ctg gtt cca acc gac gtg act gca cgt atg gtt gct 307
Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
              55              60              65

tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
              70              75              80              85

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
              90              95              100

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
              105              110              115

gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
              120              125              130

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
              135              140              145

cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
              150              155              160              165

ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu Lys Ala Leu Gly Lys
              170              175              180

taagatttct tctctagtgc tgc 666

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<210> 964  
<211> 181  
<212> PRT  
<213> *Corynebacterium glutamicum*

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<400> 964
Met Arg Leu Val Leu Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln
  1           5           10           15
Ala Ala Ile Leu Ser Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly
  20           25           30
Asp Leu Phe Arg Ala Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu
  35           40           45
Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr
  50           55           60
Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly
  65           70           75           80
Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu
  85           90           95
Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn
  100          105          110
Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly
  115          120          125
Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr
  130          135          140
Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile
  145          150          155          160
Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu
  165          170          175
Lys Ala Leu Gly Lys
  180

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<210> 965
<211> 531
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(508)  
<223> RXA00266
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<400> 965
agtaggggat cgtccagcga agcggtcgca gaggctgtga ggaagctcta agtcgactta 60
agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115
              Met Thr Glu Arg Thr
              1              5

```

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163  
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu  
                   10                                  15                                  20

atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211  
 Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp  
                   25                                  30                                  35

ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259  
 Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His  
                   40                                  45                                  50

gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307  
 Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala  
                   55                                  60                                  65

cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355  
 Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp  
                   70                                  75                                  80                                  85

cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403  
 Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly  
                   90                                  95                                  100

acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451  
 Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His  
                   105                                  110                                  115

ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499  
 Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe  
                   120                                  125                                  130

cct aac ctg taatttttac ggtagaaaa aaa 531  
 Pro Asn Leu  
                   135

&lt;210&gt; 966

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 966

Met Thr Glu Arg Thr Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn  
           1                                  5                                  10                                  15

Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys  
                   20                                  25                                  30

Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys  
                   35                                  40                                  45

His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu  
                   50                                  55                                  60

Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg  
                   65                                  70                                  75                                  80

Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala  
                   85                                  90                                  95

Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly  
                   100                  105                  110

Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu  
                   115                  120                  125

Ile Ser Ile Trp Phe Pro Asn Leu  
           130                  135

&lt;210&gt; 967

&lt;211&gt; 1245

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1222)

&lt;223&gt; RXA00489

&lt;400&gt; 967

cagcccgatt tcttcattga aatcgggctg tttctgggtg tgtcgcgtat ctcgggtaaa 60

gtcttcgtcg tatacgacca tttaaggag gcccgtcaca atg cgt gac cac gtt 115  
   Met Arg Asp His Val  
   1                  5

gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163  
  Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr Tyr Ser Leu Asp Asp  
                                   10                  15                  20

att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211  
  Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp  
                                   25                  30                  35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat 259  
  Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn  
                                   40                  45                  50

cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc 307  
  His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly  
                                   55                  60                  65

aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc 355  
  Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg  
                                   70                  75                  80                  85

cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag 403  
  His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu  
                                   90                  95                  100

gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca 451  
  Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala  
                                   105                  110                  115

gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt 499  
  Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg  
                                   120                  125                  130

gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt 547  
  Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg

135	140	145	
gag atc gca cca atc gtc atc aag gca ggt gct gat ctg ctg gtt atc			595
Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala Asp Leu Leu Val Ile			
150	155	160	165
cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc			643
Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala			
	170	175	180
ctg aac cta aag gaa ttc atc ggt tct ttg gat gtt cct gtc atc gct			691
Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp Val Pro Val Ile Ala			
	185	190	195
ggg ggc gtg aac gat tac acc acc gcg ttg cac atg atg cgt acc ggt			739
Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His Met Met Arg Thr Gly			
	200	205	210
gct gtg ggc atc atc gtc ggt ggc ggc gag aac acc aac agc cta gca			787
Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn Thr Asn Ser Leu Ala			
	215	220	225
ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg			835
Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala			
	230	235	240
gca cgt cgt gat tac ctg gat gag acc ggt gga cgt tac gtg cac atc			883
Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly Arg Tyr Val His Ile			
	250	255	260
att gca gat gga agc att gaa aac tcc ggt gat gta gtc aag gct att			931
Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp Val Val Lys Ala Ile			
	265	270	275
gcc tgt ggc gca gat gct gtg gtg ctg ggt tca ccg ttg gct cgc gct			979
Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser Pro Leu Ala Arg Ala			
	280	285	290
gaa gaa gct gct gga aag ggc tac ttc tgg cca gca gtg gca gcg cac			
1027			
Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro Ala Val Ala Ala His			
	295	300	305
cct cgt ttc cca cgc ggt gtg gtt act gag tcc gtg gac ttg gat gag			
1075			
Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser Val Asp Leu Asp Glu			
	310	315	320
gca gca cca agc ttg gag cag att ctg cat ggt ccg tct acg atg ccg			
1123			
Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly Pro Ser Thr Met Pro			
	330	335	340
tgg ggt gtg gaa aac ttc gaa ggt gga tta aag cgt gcg ctg gct aag			
1171			
Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys Arg Ala Leu Ala Lys			
	345	350	355
tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt			
1219			
Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys Val Ser Leu His Val			

360

365

370

aac taggtgtgtg tactcgctc ttc  
1245  
Asn

&lt;210&gt; 968

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 968

Met Arg Asp His Val Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr  
1 5 10 15

Tyr Ser Leu Asp Asp Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser  
20 25 30

Ser Lys Asp Val Asp Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp  
35 40 45

Leu Pro Phe Met Asn His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe  
50 55 60

Val Ile Glu Met Gly Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu  
65 70 75 80

Gly Leu Trp Gly Arg His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val  
85 90 95

Ile Ala Ala Tyr Glu Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu  
100 105 110

Gln Glu Leu His Ala Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg  
115 120 125

Ile Ala Gln Val Arg Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser  
130 135 140

Pro Gln Asn Val Arg Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala  
145 150 155 160

Asp Leu Leu Val Ile Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn  
165 170 175

Thr Gly Gly Glu Ala Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp  
180 185 190

Val Pro Val Ile Ala Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His  
195 200 205

Met Met Arg Thr Gly Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn  
210 215 220

Thr Asn Ser Leu Ala Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile  
225 230 235 240

Ala Asp Val Ala Ala Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly  
245 250 255

Arg Tyr Val His Ile Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp  
 260 265 270

Val Val Lys Ala Ile Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser  
 275 280 285

Pro Leu Ala Arg Ala Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro  
 290 295 300

Ala Val Ala Ala His Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser  
 305 310 315 320

Val Asp Leu Asp Glu Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly  
 325 330 335

Pro Ser Thr Met Pro Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys  
 340 345 350

Arg Ala Leu Ala Lys Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys  
 355 360 365

Val Ser Leu His Val Asn  
 370

<210> 969  
 <211> 1545  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1531)  
 <223> RXN02281

<400> 969  
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cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115  
 Val Gln Lys Asp Ser  
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211  
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355  
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg

70	75	80	85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat				403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn				
	90	95	100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg				451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro				
	105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt				499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly				
	120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac				547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp				
	135	140	145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg				595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro				
	150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc				643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile				
	170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg				691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu				
	185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg				739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met				
	200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca				787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro				
	215	220	225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa				835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu				
	230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc				883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile				
	250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca				931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro				
	265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa				979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu				
	280	285	290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc				
1027				
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg				
	295	300	305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att				
1075				



Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile  
 310 315 320 325  
 ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
 1123  
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
 330 335 340  
 atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac  
 1171  
 Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp  
 345 350 355  
 aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac  
 1219  
 Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn  
 360 365 370  
 tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc  
 1267  
 Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser  
 375 380 385  
 acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga  
 1315  
 Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly  
 390 395 400 405  
 tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg  
 1363  
 Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu  
 410 415 420  
 cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac  
 1411  
 Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr  
 425 430 435  
 ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa  
 1459  
 Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu  
 440 445 450  
 tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg  
 1507  
 Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg  
 455 460 465  
 acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga  
 1545  
 Thr Leu Gly Glu Val Pro Phe Arg  
 470 475  
 <210> 970  
 <211> 477  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 970  
 Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp

1	5	10	15
Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala	20	25	30
Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val	35	40	45
Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg	50	55	60
Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr	65	70	75
Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu	85	90	95
Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp	100	105	110
Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu	115	120	125
Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu	130	135	140
Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn	145	150	155
Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile	165	170	175
Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val	180	185	190
Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe	195	200	205
Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val	210	215	220
Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr	225	230	235
Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro	245	250	255
Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn	260	265	270
Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala	275	280	285
Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met	290	295	300
Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln	305	310	315
Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile	325	330	335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
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Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser  
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Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn  
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Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr  
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Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu  
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Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln  
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Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala  
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Val	Ile	Glu	Arg	Tyr	Leu	Arg	Glu	Gln	Leu	Glu	Arg	Leu	Thr	Ser	Asn	
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Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro	
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Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly	
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Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp	
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Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met	
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Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu	
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Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg	
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1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
330 335 340

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Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
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Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
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Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
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Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
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Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
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Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
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Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
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Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
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Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
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Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
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 Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile  
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Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe	
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Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe	
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Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe	
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Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly	
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cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883
Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu	
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gtt	ctt	gaa	gcc	gac	att	cca	ttc	ttt	ggc	atc	tgc	ttc	ggc	aac	cag	931
Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn	Gln	
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 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile  
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 1123  
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys  
 330                      335                      340  
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 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala  
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 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala  
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 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln  
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 Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr  
 35                      40                      45  
 Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg  
 50                      55                      60  
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn  
 65                      70                      75                      80  
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu  
 85                      90                      95



Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr  
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 130 135 140  
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu  
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 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu  
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 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly  
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 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn  
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 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro  
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 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val  
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 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val  
 245 250 255  
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 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr  
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 340 345 350  
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala  
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&lt;223&gt; RXA00145

&lt;400&gt; 975

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                                         1           5

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Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val Gly Leu Leu Asp Glu
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Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg Glu Val Lys Lys Leu
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ccc acg ctg cgt ggt cgc acc att ttt acc ttg ttc tat gag aac tcc 259
Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu Phe Tyr Glu Asn Ser
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Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly Lys Trp Met Ser Ala
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Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser Val Lys Lys Gly Glu
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Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala Ile Gly Ala Asp Ala
          90           95          100

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Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val Ile Asn Ala Gly Asp
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Gly Ser His Gln His Pro Thr Gln Ala Leu Leu Asp Ala Leu Thr Ile
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cgg cag cgc acc ggc cgc att gag gga ctc aaa gtt gtc atc gtg ggc 595
Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys Val Val Ile Val Gly
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gac tgt ttg cac tcc cgg gtg gtg cgc tcc aat gtg gat ctg ctg tcc 643
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Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro Pro Thr Leu Leu Pro

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Glu Ile Ala Asp Ala Asp Val Val Met Met Leu Arg Val Gln Gln Glu				
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Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg Glu Tyr Ala Thr Leu				
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tac ggc atg tcc aaa gag cgc gaa gct cgc ctc aag gac tcc gcc atc				883
Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu Lys Asp Ser Ala Ile				
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Ile Met His Pro Gly Pro Met Leu Arg Gly Met Glu Ile Asn Phe Gln				
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Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln Gln Val Ser Asn Gly				
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 Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser  
 195 200 205  
 Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu  
 210 215 220  
 Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg  
 225 230 235 240  
 Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu  
 245 250 255  
 Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met  
 260 265 270  
 Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln  
 275 280 285  
 Gln Val Ser Asn Gly Val His Met Arg Met Ala Ile Leu Phe Ala Leu  
 290 295 300  
 Val Ala Gly Ser Asp Ala Thr Ile  
 305 310

&lt;210&gt; 977

&lt;211&gt; 1464

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1441)

&lt;223&gt; RXA00146

&lt;400&gt; 977

atggccattt tgttcgccct ggctgcaggc tctgacgcga ctatctaate gcgaccatct 60

gatcgcgaaa ttctagaaaa ggtaacgagg gattaaagaa gtg gtt gac agc aac 115  
 Val Val Asp Ser Asn  
 1 5

acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca 163

Thr	Gln	Tyr	Pro	Glu	Thr	Gly	Ala	Leu	Ala	Pro	Ala	Pro	Ala	Asp	Ser		
				10					15					20			
ctc	cta	atc	agc	aac	gtt	ttg	gtc	tac	ggc	gaa	ggc	gag	cca	acg	aat	211	
Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu	Gly	Glu	Pro	Thr	Asn		
			25					30					35				
gtg	ttt	gtt	aaa	gat	ggg	gtg	atc	gca	gct	atc	ggc	ggc	act	cat	gag	259	
Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile	Gly	Gly	Thr	His	Glu		
		40					45					50					
gct	gac	cgc	acc	atc	gac	ggc	aat	ggg	gga	gtt	ctc	ctt	cca	ggg	ttc	307	
Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val	Leu	Leu	Pro	Gly	Phe		
	55					60					65						
gtg	gac	atg	cac	gtt	cac	ctg	cgt	gag	cca	ggc	cgc	gaa	gac	act	gaa	355	
Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly	Arg	Glu	Asp	Thr	Glu		
	70				75				80						85		
acc	att	gcc	act	ggg	tct	gcc	gcc	gca	gcc	aag	ggc	gga	ttc	acc	gca	403	
Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys	Gly	Gly	Phe	Thr	Ala		
				90				95					100				
gta	ttc	acc	atg	gcg	aac	acc	act	cca	gtg	atg	gat	cag	ccg	gtt	atc	451	
Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met	Asp	Gln	Pro	Val	Ile		
			105					110				115					
gcg	gaa	tcc	gta	tgg	ttc	aag	ggc	caa	aac	att	ggc	ctg	tgc	gac	gtg	499	
Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile	Gly	Leu	Cys	Asp	Val		
		120					125					130					
cat	cca	gtt	gga	tcc	atc	acc	aag	ggg	ctt	gag	ggc	aag	gag	ctt	act	547	
His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu	Gly	Lys	Glu	Leu	Thr		
	135					140					145						
gag	ttc	ggc	atg	atg	gct	cgc	tct	gaa	gcc	aag	gtg	cgc	atg	ttc	tct	595	
Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys	Val	Arg	Met	Phe	Ser		
	150				155					160				165			
gat	gat	ggc	aag	tgc	gtc	gat	gat	cct	cag	gtc	atg	cgc	cgc	gcg	ctg	643	
Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val	Met	Arg	Arg	Ala	Leu		
			170					175						180			
gaa	tac	gcc	aag	ggc	atg	gac	gtt	ttg	atc	gcc	cag	cac	gct	gag	gat	691	
Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala	Gln	His	Ala	Glu	Asp		
		185						190					195				
cac	cgc	ctg	act	gag	ggc	gct	tca	gca	cac	gag	ggg	gaa	aac	gca	gct	739	
His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu	Gly	Glu	Asn	Ala	Ala		
		200					205					210					
cgt	ctg	ggg	ctg	cgc	ggc	tgg	cca	cgt	gtg	gct	gag	gaa	tcc	atc	gtg	787	
Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala	Glu	Glu	Ser	Ile	Val		
	215					220					225						
gtg	cgc	gat	gcc	atc	atg	gct	cgt	gac	tac	ggc	aac	cgc	gtg	cac	atc	835	
Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly	Asn	Arg	Val	His	Ile		
	230				235					240				245			
tgc	cac	gcc	tcc	act	gaa	ggc	acc	gtg	gag	ttg	ctt	cgt	tgg	gct	aag	883	
Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu	Leu	Arg	Trp	Ala	Lys		

250	255	260	
tcc cag ggc att cca atc acc gcg gaa gtc acc ccg cac cac ctc acc			931
Ser Gln Gly Ile Pro Ile Thr Ala Glu Val Thr Pro His His Leu Thr			
265	270	275	
ttg acc gat gag cgc ctg gaa acc tac gac gcg gtc aac aaa gtc aat			979
Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala Val Asn Lys Val Asn			
280	285	290	
ccg cca ctg cgc gaa agc cgc gat gcc gaa gcg ctc aag aag gcg ctt			
1027			
Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala Leu Lys Lys Ala Leu			
295	300	305	
ctc gac ggc acc atc gat gtt gtt gca acc gac cac gct cct cac ggt			
1075			
Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp His Ala Pro His Gly			
310	315	320	325
tcc gaa gat aag tgc tgt gaa ttc gaa aac gcc aag cca ggc atg ctc			
1123			
Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala Lys Pro Gly Met Leu			
330	335	340	
gga ttg gaa acc tca ctg tcc atc atc gtg gac acc ttc gtt gcc acc			
1171			
Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp Thr Phe Val Ala Thr			
345	350	355	
gga ctt gca gac tgg cgc ttt gtt gcg cgc gtg atg agt gaa cgc cca			
1219			
Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val Met Ser Glu Arg Pro			
360	365	370	
gca gaa atc acc cgt cta cca ggc cag ggt cgc cca atc gca gaa ggt			
1267			
Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg Pro Ile Ala Glu Gly			
375	380	385	
gag cca gca aac ctc gcg att gtt gat cca gga aaa acc tgg aca gca			
1315			
Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly Lys Thr Trp Thr Ala			
390	395	400	405
tcc ggt gca gac ttt gcg tcc aag gct gaa aat acc cca ttt gag ggc			
1363			
Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn Thr Pro Phe Glu Gly			
410	415	420	
caa gaa ttc agt gcc aag gtc aca cac acc gtg ctt cgt ggc aag gtg			
1411			
Gln Glu Phe Ser Ala Lys Val Thr His Thr Val Leu Arg Gly Lys Val			
425	430	435	
act tgt gca gac gga gtt gca caa aac gct taacgggtgg gtgcatagta			
1461			
Thr Cys Ala Asp Gly Val Ala Gln Asn Ala			
440	445		

tgc  
1464

<210> 978  
<211> 447  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 978

Val	Val	Asp	Ser	Asn	Thr	Gln	Tyr	Pro	Glu	Thr	Gly	Ala	Leu	Ala	Pro
1				5					10					15	
Ala	Pro	Ala	Asp	Ser	Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu
			20					25					30		
Gly	Glu	Pro	Thr	Asn	Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile
		35					40					45			
Gly	Gly	Thr	His	Glu	Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val
	50					55					60				
Leu	Leu	Pro	Gly	Phe	Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly
65					70					75					80
Arg	Glu	Asp	Thr	Glu	Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys
				85					90						95
Gly	Gly	Phe	Thr	Ala	Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met
			100					105					110		
Asp	Gln	Pro	Val	Ile	Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile
		115						120				125			
Gly	Leu	Cys	Asp	Val	His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu
	130					135					140				
Gly	Lys	Glu	Leu	Thr	Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys
145					150					155					160
Val	Arg	Met	Phe	Ser	Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val
				165					170					175	
Met	Arg	Arg	Ala	Leu	Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala
			180					185					190		
Gln	His	Ala	Glu	Asp	His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu
		195					200					205			
Gly	Glu	Asn	Ala	Ala	Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala
	210					215					220				
Glu	Glu	Ser	Ile	Val	Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly
225					230					235					240
Asn	Arg	Val	His	Ile	Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu
			245						250					255	
Leu	Arg	Trp	Ala	Lys	Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr
			260				265						270		

Pro His His Leu Thr Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala  
 275 280 285

Val Asn Lys Val Asn Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala  
 290 295 300

Leu Lys Lys Ala Leu Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp  
 305 310 315 320

His Ala Pro His Gly Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala  
 325 330 335

Lys Pro Gly Met Leu Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp  
 340 345 350

Thr Phe Val Ala Thr Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val  
 355 360 365

Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg  
 370 375 380

Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly  
 385 390 395 400

Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn  
 405 410 415

Thr Pro Phe Glu Gly Gln Glu Phe Ser Ala Lys Val Thr His Thr Val  
 420 425 430

Leu Arg Gly Lys Val Thr Cys Ala Asp Gly Val Ala Gln Asn Ala  
 435 440 445

&lt;210&gt; 979

&lt;211&gt; 1025

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1002)

&lt;223&gt; RXA02208

&lt;400&gt; 979

ctc gga gtc gtc gac ggc gtc gca cct cta aac cgc acc atg gaa aaa	48
Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys	
1 5 10 15	
atc atc gca gtg cac gat gat tcc ctc tcc cag gaa gtc ttc ggc gtc	96
Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val	
20 25 30	
acc ttc cca cga cca cta ggc ctc gcc gca ggt ttc gac aaa aac gca	144
Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala	
35 40 45	
tca atg gct gat gcc tgg ggt gcc gtt gga ttc gga tac gcc gaa ctt	192
Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu	
50 55 60	



ggc acc gtc acc gcc ttc cca cag cca gga aac ccc acc ccg cgc ctt	240
Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu	
65 70 75 80	
ttc cgc ctg cct gcc gac aaa gct atc ttg aac cgc atg gga ttc aac	288
Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn	
85 90 95	
aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc	336
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser	
100 105 110	
acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct	384
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala	
115 120 125	
gaa cac gca gta gat gac tac cgc cgt tct gca tct ttg tta ggt gat	432
Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp	
130 135 140	
ctt gct gat tac ctg gtt gtc aac gtt tcc tcc ccc aac act ccg ggt	480
Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly	
145 150 155 160	
ctc cgc gat ctg cag gct gtg gaa tct ttg cga cca atc ctc gcc gca	528
Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala	
165 170 175	
gtg cag gaa tcc acc acc gtc cca gtc ttg gtg aaa atc gca cca gac	576
Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp	
180 185 190	
ctc tcc gac gaa gac atc gac gcc gta gct gac ctg gca gtt gag ctc	624
Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu	
195 200 205	
aaa ctc gcc gga atc gta gcc acc aat acc acc att tcc cgc gaa ggc	672
Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly	
210 215 220	
ctc aac act cct tca ggt gaa gtc gaa gcc atg ggt gct ggc gga atc	720
Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile	
225 230 235 240	
tcc ggt gct cca gta gca gcc cga tct ttg gag gta ctc aag cgc ctc	768
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	
245 250 255	
tac gca cgg gta ggc aaa gag atg gtg ttg atc tct gtc ggt ggc atc	816
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	
260 265 270	
agc acc cct gag caa gcc tgg gaa cgc atc acc tcc ggc gca acc ctt	864
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	
275 280 285	
ctg cag gga tac acc cca ttc atc tac ggt ggc ccc gat tgg atc aga	912
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	
290 295 300	
gat atc cac ctt ggt atc gcc aag cag ctg aaa gct cac ggt ctg cgc	960

Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg  
 305 310 315 320

aac atc gct gac gct gtg ggc agc gaa ttg gag tgg aag aac  
 1002

Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn  
 325 330

taaacagacc aaacacacgt gcc  
 1025

<210> 980

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 980

Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys  
 1 5 10 15

Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val  
 20 25 30

Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala  
 35 40 45

Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu  
 50 55 60

Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu  
 65 70 75 80

Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn  
 85 90 95

Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser  
 100 105 110

Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala  
 115 120 125

Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp  
 130 135 140

Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly  
 145 150 155 160

Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala  
 165 170 175

Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp  
 180 185 190

Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu  
 195 200 205

Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly  
 210 215 220

Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile

225	230	235	240
Ser Gly Ala Pro Val	Ala Ala Arg Ser	Leu Glu Val Leu Lys Arg Leu	
	245	250	255
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile			
	260	265	270
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu			
	275	280	285
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg			
	290	295	300
Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg			
	305	310	315
Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn			
	325	330	

<210> 981  
 <211> 675  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(652)  
 <223> RXA01660

<400> 981  
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taaacctcaa tcatcaaatt agggaagggc tgggaaatcc atg tca tct aat tcc 115  
 Met Ser Ser Asn Ser  
 1 5

att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta 163  
 Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu Leu Ile Lys Glu Leu  
 10 15 20

gct gtc gtc cac ggt gaa gtc acc ttg tct tcg ggc aag aag gct gat 211  
 Ala Val Val His Gly Glu Val Thr Leu Ser Ser Gly Lys Lys Ala Asp  
 25 30 35

tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc 259  
 Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His Ala Arg Ala Ser Arg  
 40 45 50

ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac 307  
 Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala Asp Trp Asp Tyr Asp  
 55 60 65

gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc 355  
 Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro Val Ala Thr Ala Ile  
 70 75 80 85

atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag 403  
 Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe Val Val Arg Lys Glu  
 90 95 100

gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg 451  
 Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr  
 105 110 115  
 ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc 499  
 Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser  
 120 125 130  
 cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg 547  
 Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val  
 135 140 145  
 ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc 595  
 Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile  
 150 155 160 165  
 gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt 643  
 Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu Gly Leu Ser Asp Leu  
 170 175 180  
 gga ctc aac taacaccccc ggccccacgg agt 675  
 Gly Leu Asn

&lt;210&gt; 982

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 982

Met Ser Ser Asn Ser Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu  
 1 5 10 15  
 Leu Ile Lys Glu Leu Ala Val Val His Gly Glu Val Thr Leu Ser Ser  
 20 25 30  
 Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His  
 35 40 45  
 Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala  
 50 55 60  
 Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro  
 65 70 75 80  
 Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe  
 85 90 95  
 Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu  
 100 105 110  
 Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr  
 115 120 125  
 Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala  
 130 135 140  
 Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly  
 145 150 155 160

Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu  
 165 170 175

Gly Leu Ser Asp Leu Gly Leu Asn  
 180

<210> 983

<211> 957

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(934)

<223> RXA02235

<400> 983

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cgctgcagga actcgaccac gcagtcaagg cttaagccct atg aca ttc ggc gag 115  
 Met Thr Phe Gly Glu  
 1 5

aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att 163  
 Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile  
 10 15 20

gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta 211  
 Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val  
 25 30 35

gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac 259  
 Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp  
 40 45 50

acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt 307  
 Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly  
 55 60 65

tcc gct ggc ttt gcc atc ttg gaa gaa acc att cag acg ctg cgt gag 355  
 Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu  
 70 75 80 85

cgt ggc tgt ttg gtg gtc tct gac gcc aaa cgc ggc gat att ggc tcc 403  
 Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg Gly Asp Ile Gly Ser  
 90 95 100

acc atg gct ggc tat gcc tca gcg tgg tta gat cca gcg tca ccg ctg 451  
 Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu  
 105 110 115

tct agc gac gct gtg acg gtc tct ccc tac ctt ggt ttt cat tcc ttg 499  
 Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu  
 120 125 130

gac cca gtg ttc gaa ctt gcc gag caa cac ggc agg gga gtg ttt gtc 547  
 Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val  
 135 140 145

ttg gcc gcg acc tca aac cct gag gcc cgc gaa ctc cag gac cag caa 595  
 Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln  
 150 155 160 165  
  
 aac gct gac ggc gtg agc att tcc cag cag atc gtg gat cag gca gcg 643  
 Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala  
 170 175 180  
  
 gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc 691  
 Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys Ala Gly Asn Ile Gly  
 185 190 195  
  
 gtc gtc atc ggc gcc acc ttg tcc aaa cca cca cgc tta tcg acg ctc 739  
 Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu  
 200 205 210  
  
 ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca 787  
 Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala  
 215 220 225  
  
 agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835  
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro  
 230 235 240 245  
  
 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883  
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met  
 250 255 260  
  
 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931  
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg  
 265 270 275  
  
 tca tagtcgcgga aacggccctt aat 957  
 Ser

&lt;210&gt; 984

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 984

Met Thr Phe Gly Glu Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg  
 1 5 10 15  
  
 Leu Cys Val Gly Ile Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly  
 20 25 30  
  
 Leu Pro Val Asn Val Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val  
 35 40 45  
  
 Glu Ala Phe Ala Asp Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe  
 50 55 60  
  
 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile  
 65 70 75 80  
  
 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg  
 85 90 95

Gly Asp Ile Gly Ser Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp  
 100 105 110  
 Pro Ala Ser Pro Leu Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu  
 115 120 125  
 Gly Phe His Ser Leu Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly  
 130 135 140  
 Arg Gly Val Phe Val Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu  
 145 150 155 160  
 Leu Gln Asp Gln Gln Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile  
 165 170 175  
 Val Asp Gln Ala Ala Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys  
 180 185 190  
 Ala Gly Asn Ile Gly Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro  
 195 200 205  
 Arg Leu Ser Thr Leu Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala  
 210 215 220  
 Gln Gly Gly Thr Ala Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala  
 225 230 235 240  
 His Leu Ala Phe Pro Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro  
 245 250 255  
 Asp Ile Ala Glu Met Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe  
 260 265 270  
 Pro Gly Phe Pro Arg Ser  
 275

<210> 985  
 <211> 852  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(829)  
 <223> RXN01892

<400> 985  
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 Val Thr Thr Ser Ser  
 1 5  
 gaa caa ccc cgt aca gga tac aag cga gtg atg tta aag ctc gga ggt 163  
 Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Gly Gly  
 10 15 20  
 gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta gac 211  
 Glu Met Phe Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp  
 25 30 35

aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag att	259
Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu Ile	
40 45 50	
gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt cag	307
Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln	
55 60 65	
cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc ggc	355
Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly	
70 75 80 85	
aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat ggc	403
Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly	
90 95 100	
gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca gaa	451
Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala Glu	
105 110 115	
cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc gtt	499
Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg Val	
120 125 130	
gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac acc	547
Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp Thr	
135 140 145	
act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg atg	595
Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu Met	
150 155 160 165	
gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac cca	643
Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn Pro	
170 175 180	
gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag aag	691
Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu Lys	
185 190 195	
ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac aac	739
Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp Asn	
200 205 210	
aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att gct	787
Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile Ala	
215 220 225	
cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc	829
Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser	
230 235 240	
tgatacattt agtcttataa aca	852

&lt;210&gt; 986

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 986

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met  
 1 5 10 15  
 Leu Lys Leu Gly Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp  
 20 25 30  
 Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys  
 35 40 45  
 Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg  
 50 55 60  
 Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr  
 65 70 75 80  
 Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe  
 85 90 95  
 Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met  
 100 105 110  
 Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu  
 115 120 125  
 Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr  
 130 135 140  
 Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys  
 145 150 155 160  
 Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp  
 165 170 175  
 Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys  
 180 185 190  
 Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser  
 195 200 205  
 Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr  
 210 215 220  
 Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu  
 225 230 235 240  
 Val Glu Ser

&lt;210&gt; 987

&lt;211&gt; 798

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (47)..(775)

&lt;223&gt; FRXA01892

&lt;400&gt; 987

atgttaaaag cggttggcac aaccctact gaaggagaac accacggtg acc acc tcg 58  
Val Thr Thr Ser  
1

agt gaa caa ccc cgt aca gga tac aaa cga gtg atg tta aag ctc gaa 106  
Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Glu  
5 10 15 20

ggg gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta 154  
Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val  
25 30 35

gac aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag 202  
Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu  
40 45 50

att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250  
Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu  
55 60 65

cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298  
Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu  
70 75 80

ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346  
Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His  
85 90 95 100

ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394  
Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala  
105 110 115

gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442  
Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg  
120 125 130

gtt gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac 490  
Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp  
135 140 145

acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538  
Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu  
150 155 160

atg gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac 586  
Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn  
165 170 175 180

cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634  
Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu  
185 190 195

aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682  
Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp  
200 205 210

aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730  
Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile  
215 220 225

gct cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 775

Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser  
 230 235 240

tgatacattt agtcttataa aca

798

<210> 988

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 988

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met  
 1 5 10 15

Leu Lys Leu Glu Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp  
 20 25 30

Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys  
 35 40 45

Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg  
 50 55 60

Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr  
 65 70 75 80

Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe  
 85 90 95

Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met  
 100 105 110

Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu  
 115 120 125

Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr  
 130 135 140

Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys  
 145 150 155 160

Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp  
 165 170 175

Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys  
 180 185 190

Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser  
 195 200 205

Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr  
 210 215 220

Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu  
 225 230 235 240

Val Glu Ser

<400> 989																
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cgaggagaat	ggaacttact	aacgctgtta	tgatgacggc	atg	act	ggt	cca	acg	115							
				Met	Thr	Val	Pro	Thr								
				1				5								
cct	tat	gaa	gac	ctt	ctt	cgg	aag	att	gct	gaa	gaa	ggg	tcc	cac	aag	163
Pro	Tyr	Glu	Asp	Leu	Leu	Arg	Lys	Ile	Ala	Glu	Glu	Gly	Ser	His	Lys	
				10					15					20		
gac	gac	cgc	acc	ggc	acc	ggc	act	act	tct	tta	ttc	gga	caa	caa	atc	211
Asp	Asp	Arg	Thr	Gly	Thr	Gly	Thr	Thr	Ser	Leu	Phe	Gly	Gln	Gln	Ile	
			25					30					35			
cgc	ttt	gat	ctc	aat	gaa	ggc	ttt	ccc	ctt	ctg	acc	acc	aag	aag	gtc	259
Arg	Phe	Asp	Leu	Asn	Glu	Gly	Phe	Pro	Leu	Leu	Thr	Thr	Lys	Lys	Val	
		40					45					50				
cat	ttc	cac	tct	ggt	gtg	ggc	gag	ctt	ttg	tgg	ttc	ctt	cag	ggg	gat	307
His	Phe	His	Ser	Val	Val	Gly	Glu	Leu	Leu	Trp	Phe	Leu	Gln	Gly	Asp	
	55					60					65					
tcc	aac	gtc	aaa	tgg	ctg	cag	gat	aac	aac	atc	cgc	att	tgg	aat	gaa	355
Ser	Asn	Val	Lys	Trp	Leu	Gln	Asp	Asn	Asn	Ile	Arg	Ile	Trp	Asn	Glu	
	70				75					80					85	
tgg	gca	gat	gag	gac	ggc	gag	ctg	ggc	cct	ggt	tat	ggt	gtc	cag	tgg	403
Trp	Ala	Asp	Glu	Asp	Gly	Glu	Leu	Gly	Pro	Val	Tyr	Gly	Val	Gln	Trp	
				90				95					100			
cgt	tct	tgg	cca	acc	cct	gat	ggc	cgt	cac	att	gac	cag	atc	tca	ggc	451
Arg	Ser	Trp	Pro	Thr	Pro	Asp	Gly	Arg	His	Ile	Asp	Gln	Ile	Ser	Gly	
			105				110					115				
gct	tta	gaa	act	ctg	cga	aac	aac	cct	gat	tca	cgt	cgc	aat	att	gtc	499
Ala	Leu	Glu	Thr	Leu	Arg	Asn	Asn	Pro	Asp	Ser	Arg	Arg	Asn	Ile	Val	
	120					125						130				
tgc	gcg	tgg	aat	ggt	tcc	gag	ctt	gaa	aac	atg	gct	ctt	ccc	cct	tgt	547
Ser	Ala	Trp	Asn	Val	Ser	Glu	Leu	Glu	Asn	Met	Ala	Leu	Pro	Pro	Cys	
	135					140					145					
cac	ttg	ctt	ttc	cag	ctc	tat	gtc	gcc	gat	ggc	aaa	ctg	tct	tgc	cag	595
His	Leu	Leu	Phe	Gln	Leu	Tyr	Val	Ala	Asp	Gly	Lys	Leu	Ser	Cys	Gln	
	150				155				160					165		
ctc	tac	cag	cgt	tct	gcg	gac	atg	ttc	ctg	ggc	gtg	cct	ttc	aac	atc	643
Leu	Tyr	Gln	Arg	Ser	Ala	Asp	Met	Phe	Leu	Gly	Val	Pro	Phe	Asn	Ile	
				170					175					180		

gca tct tat gca ctg ctc acc cac atg ttt gcc cag cag gca ggc ttg 691  
 Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala Gln Gln Ala Gly Leu  
                   185                                  190                                  195

gaa gtc ggc gag ttc att tgg act ggc ggc gac tgc cac att tat gac 739  
 Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp Cys His Ile Tyr Asp  
                   200                                  205                                  210

aac cac aag gaa cag gtc gcg gag cag ctg agc cga taagctcgcc 785  
 Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser Arg  
                   215                                  220                                  225

cctacccccac ctt 798

<210> 990

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 990

Met Thr Val Pro Thr Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu  
   1                                  5                                  10                                  15

Glu Gly Ser His Lys Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu  
                   20                                  25                                  30

Phe Gly Gln Gln Ile Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu  
                   35                                  40                                  45

Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp  
                   50                                  55                                  60

Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile  
   65                                  70                                  75                                  80

Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val  
                   85                                  90                                  95

Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile  
                   100                                  105                                  110

Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser  
                   115                                  120                                  125

Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met  
                   130                                  135                                  140

Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly  
   145                                  150                                  155                                  160

Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly  
                   165                                  170                                  175

Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala  
                   180                                  185                                  190

Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp  
                   195                                  200                                  205

Cys His Ile Tyr Asp Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser

210

215

220

Arg  
225

&lt;210&gt; 991

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(709)

&lt;223&gt; RXA00131

&lt;400&gt; 991

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aggctctcgg cggtcagctc accgaactga ccaaggagca ggctgagtac atcggcggttg 60

acgttgcagg cccattcaag ccggagcact accgctacta atg att gtc agc att 115
                                         Met Ile Val Ser Ile
                                         1                               5

gag gga atc gac ggc gcc ggc aaa aac acc ctg gtt tcg gca tta acg 163
Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr
                        10                               15                               20

cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser
                        25                               30                               35

att cac gcc caa ttg gcc gcg gaa gca ctc cac ggc cgc atg ggc gac 259
Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp
                        40                               45                               50

ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg
                        55                               60                               65

cac ttc gcg att gat gac tta aat gcg ccc ggc gtg gtg ctg ctc gac 355
His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp
                        70                               75                               80                               85

cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp
                        90                               95                               100

gac gac gcc ccc cgc tgg gtt gcc gac ctg gaa ttc ggg cgg ctt ggg 451
Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly
                        105                               110                               115

ctc cca cgt ccg acg ctt caa gtg ttg ttg gat acc ccc gcg gag gta 499
Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val
                        120                               125                               130

gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547
Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala
                        135                               140                               145

cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu

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150	155	160	165	
cac tat cgc cgc ctc gcg gcg gac aac tgg gaa tca ccg tgg atc gtg				643
His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val	170	175	180	
ggt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa				691
Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu	185	190	195	
ttc ctg ggt act ata aac taatcccaat tagcaggaag gat				732
Phe Leu Gly Thr Ile Asn	200			

&lt;210&gt; 992

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 992

Met Ile Val Ser Ile Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu	1	5	10	15
Val Ser Ala Leu Thr Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro	20	25	30	
Arg Tyr Glu Thr Ser Ile His Ala Gln Leu Ala Ala Glu Ala Leu His	35	40	45	
Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu	50	55	60	
Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly	65	70	75	80
Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala	85	90	95	
Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu	100	105	110	
Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp	115	120	125	
Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu	130	135	140	
Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln	145	150	155	160
Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu	165	170	175	
Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala	180	185	190	
Gln Arg Ile Val Glu Phe Leu Gly Thr Ile Asn	195	200		

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<220>  
<221> CDS  
<222> (101)..(508)  
<223> RXA00266
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<210> 994
<211> 136
<212> PRT
<213> Corynebacterium glutamicum
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1362



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	20	25	30
Leu Ala Ala	Leu Asp Leu Arg Val	Ala Asp Arg Glu Thr	Ala Glu Lys
	35	40	45
His Tyr Glu	Glu His Ala Asp Lys	Pro Phe Phe Gly	Glu Leu Val Glu
	50	55	60
Phe Ile Thr	Ser Ala Pro Leu Ile	Ala Gly Ile Val	Glu Gly Glu Arg
	65	70	75
Ala Ile Asp	Ala Trp Arg Gln Leu	Ala Gly Gly Thr	Asp Pro Val Ala
	85	90	95
Lys Ala Thr	Pro Gly Thr Ile Arg	Gly Asp Phe Ala	Leu Thr Val Gly
	100	105	110
Glu Asn Val	Val His Gly Ser Asp	Ser Pro Glu Ser	Ala Glu Arg Glu
	115	120	125
Ile Ser Ile	Trp Phe Pro Asn	Leu	
	130	135	

&lt;210&gt; 995

&lt;211&gt; 831

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(808)

&lt;223&gt; RXA00718

&lt;400&gt; 995

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                                   Val Thr Glu Ile Ser
                                   1           5
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Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly
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Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala
                                   25           30           35
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Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val
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Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala
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 Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala Lys Ala His Arg Cys  
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 Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val Arg Ala Gln Arg Arg  
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 Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val Asp Phe Asp Ala Val  
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 Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile Val Asp Thr Ser Asp  
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 atg acc atg gat caa gta ctt gat cac ctc atc cac cta gtg gaa gcc 787  
 Met Thr Met Asp Gln Val Leu Asp His Leu Ile His Leu Val Glu Ala  
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&lt;210&gt; 996

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 996

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 Asp Gly Pro Ser Gly Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala  
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 Thr Arg Leu Ser Ala Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val  
 35 40 45  
 Ala Thr Leu His Val Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala  
 50 55 60

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp  
65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp  
85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile  
100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala  
115 120 125

Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val  
130 135 140

Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val  
145 150 155 160

Arg Ala Gln Arg Arg Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val  
165 170 175

Asp Phe Asp Ala Val Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp  
180 185 190

Ser Thr Arg Ala Ala Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile  
195 200 205

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His Leu Val Glu Ala Ser Ala Glu Arg Ser Asn Gln  
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Met Thr Ser Ser Arg  
1 5

aaa gtc cgt ccc acc aaa cac att ttc gtc acc ggt gga gtt gtt tcc 163  
Lys Val Arg Pro Thr Lys His Ile Phe Val Thr Gly Gly Val Val Ser  
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tca ctc ggc aaa ggc ctg acc gca gca agc ctt ggt caa ttg ctg att 211  
Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu Gly Gln Leu Leu Ile  
25 30 35

gca cgg gga ctg tcg gtg acc atg cag aag ctg gat cca tac ctc aat 259

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Val	Asp	Pro	Gly	Thr	Met	Asn	Pro	Phe	Glu	His	Gly	Glu	Val	Phe	Val	
		55				60					65					
acc	gaa	gac	ggg	gca	gaa	aca	gac	ctg	gat	ttg	ggc	cac	tac	gag	cgt	355
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
		70				75				80					85	
ttc	ctc	gat	cgc	aac	ctg	ggg	ctc	aac	gcc	aat	gtc	acc	acc	ggc	aag	403
Phe	Leu	Asp	Arg	Asn	Leu	Gly	Leu	Asn	Ala	Asn	Val	Thr	Thr	Gly	Lys	
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gtg	tat	tcc	act	gtg	atc	gcc	aag	gag	cgc	agg	gga	gag	tac	ctg	ggg	451
Val	Tyr	Ser	Thr	Val	Ile	Ala	Lys	Glu	Arg	Arg	Gly	Glu	Tyr	Leu	Gly	
			105					110						115		
aaa	act	gtg	cag	gtc	atc	cca	cac	atc	act	gat	gag	atc	aaa	gct	cgt	499
Lys	Thr	Val	Gln	Val	Ile	Pro	His	Ile	Thr	Asp	Glu	Ile	Lys	Ala	Arg	
		120					125					130				
att	ttg	agc	atg	ggc	gaa	cca	gat	gct	cat	ggg	aac	gcc	cca	gac	gtg	547
Ile	Leu	Ser	Met	Gly	Glu	Pro	Asp	Ala	His	Gly	Asn	Ala	Pro	Asp	Val	
		135				140					145					
gtg	atc	tct	gag	gtc	ggg	ggc	acc	gtc	ggg	gac	att	gaa	tcc	cag	cca	595
Val	Ile	Ser	Glu	Val	Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Gln	Pro	
		150				155				160					165	
ttc	ctt	gaa	gca	gct	cgc	cag	gta	cgc	cat	gaa	att	ggg	cgt	gaa	aac	643
Phe	Leu	Glu	Ala	Ala	Arg	Gln	Val	Arg	His	Glu	Ile	Gly	Arg	Glu	Asn	
				170					175					180		
tgc	ttc	ttc	atc	cac	tgt	tct	ttg	gtg	cca	tac	ttg	gct	acc	tca	ggg	691
Cys	Phe	Phe	Ile	His	Cys	Ser	Leu	Val	Pro	Tyr	Leu	Ala	Thr	Ser	Gly	
			185					190						195		
gag	ctg	aag	acc	aaa	ccc	acc	cag	cat	tct	gtc	gca	gag	ctg	cgc	ggc	739
Glu	Leu	Lys	Thr	Lys	Pro	Thr	Gln	His	Ser	Val	Ala	Glu	Leu	Arg	Gly	
		200					205					210				
atc	ggg	att	ttg	ccg	gat	gct	ctc	gtg	ctt	cgt	tgc	gat	cgg	gag	gtc	787
Ile	Gly	Ile	Leu	Pro	Asp	Ala	Leu	Val	Leu	Arg	Cys	Asp	Arg	Glu	Val	
		215				220					225					
cct	caa	ggg	ctg	aaa	gat	aag	atc	gcg	atg	atg	tgc	gat	ggt	gat	tat	835
Pro	Gln	Gly	Leu	Lys	Asp	Lys	Ile	Ala	Met	Met	Cys	Asp	Val	Asp	Tyr	
		230				235				240					245	
gaa	ggc	ggt	gta	tct	tgc	cct	gat	tcc	agt	tct	att	tac	aac	att	cca	883
Glu	Gly	Val	Val	Ser	Cys	Pro	Asp	Ser	Ser	Ser	Ile	Tyr	Asn	Ile	Pro	
				250					255					260		
gat	gtc	ctc	tac	cgc	gag	cac	ctg	gac	acc	ttc	att	att	cgt	cgc	ctg	931
Asp	Val	Leu	Tyr	Arg	Glu	His	Leu	Asp	Thr	Phe	Ile	Ile	Arg	Arg	Leu	
			265				270						275			
ggc	ctt	ccg	ttc	cgt	gat	ggt	gac	tgg	agc	acc	tgg	cac	gat	ctg	ctg	979
Gly	Leu	Pro	Phe	Arg	Asp	Val	Asp	Trp	Ser	Thr	Trp	His	Asp	Leu	Leu	

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Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly		
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aag tac att gat ctt ccc gat gct tat ctc tca gtg gtg gaa gct gtt		
1075		
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val		
310	315	320 325
cgc gct gca ggc tac gcc aat tgg acg cgc acc aat atc aag tgg att		
1123		
Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile		
	330	335 340
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1171		
Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala Met Lys Ala Leu Ser		
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1219		
Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe Gly Ile Arg Gly Ile		
	360	365 370
gaa ggc aaa atc ggt gcg att acg ttt gca cgt gag cac aag atc ccg		
1267		
Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg Glu His Lys Ile Pro		
	375	380 385
ctt ctt ggc cta tgc ctt ggc ctg cag tgc acc gtc atc gag gca gca		
1315		
Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr Val Ile Glu Ala Ala		
390	395	400 405
cgc cag gca gga ctg gag cag gca tca tcc act gag ttt gac cca gct		
1363		
Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr Glu Phe Asp Pro Ala		
	410	415 420
gca acg cag cca gtg atc gcc acc atg gaa gag cag aaa gct gct gtg		
1411		
Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu Gln Lys Ala Ala Val		
	425	430 435
tcg ggt gaa gct gat ctg ggt ggc acc atg cgt ctt ggc gca tat cct		
1459		
Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Tyr Pro		
	440	445 450
gca acc ctg gag gaa ggc tcc tta gta gcg gaa ctg tat ggc aca acg		
1507		
Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu Leu Tyr Gly Thr Thr		
	455	460 465
gaa gtc tcc gag cgc cac cgt cac cgc tat gag gtc aat aat gcc tac		
1555		
Glu Val Ser Glu Arg His Arg His Arg Tyr Glu Val Asn Asn Ala Tyr		
470	475	480 485

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1603

Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val Phe Ser Gly Thr Ser  
490 495 500

cct gat gga cat ttg gtg gag ttc gtg gag tac ccc aaa gag gtg cat  
1651

Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr Pro Lys Glu Val His  
505 510 515

cct tat ctg gtg gca acc cag gcg cac cct gag tac aaa tct cgt cca  
1699

Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu Tyr Lys Ser Arg Pro  
520 525 530

acc cat gct cat cca ctg ttt tac ggc ctg gtg aag acc gct ttg gag  
1747

Thr His Ala His Pro Leu Phe Tyr Gly Leu Val Lys Thr Ala Leu Glu  
535 540 545

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1785

Leu Arg Val His Pro  
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<400> 998

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Gly Gln Leu Leu Ile Ala Arg Gly Leu Ser Val Thr Met Gln Lys Leu  
35 40 45

Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His  
50 55 60

Gly Glu Val Phe Val Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu  
65 70 75 80

Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn  
85 90 95

Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg  
100 105 110

Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp  
115 120 125

Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly  
130 135 140

Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp

145	150	155	160
Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu	165	170	175
Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr	180	185	190
Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val	195	200	205
Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg	210	215	220
Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met	225	230	235
Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser	245	250	255
Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe	260	265	270
Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr	275	280	285
Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr	290	295	300
Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser	305	310	315
Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr	325	330	335
Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala	340	345	350
Met Lys Ala Leu Ser Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe	355	360	365
Gly Ile Arg Gly Ile Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg	370	375	380
Glu His Lys Ile Pro Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr	385	390	395
Val Ile Glu Ala Ala Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr	405	410	415
Glu Phe Asp Pro Ala Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu	420	425	430
Gln Lys Ala Ala Val Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg	435	440	445
Leu Gly Ala Tyr Pro Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu	450	455	460
Leu Tyr Gly Thr Thr Glu Val Ser Glu Arg His Arg His Arg Tyr Glu	465	470	475
			480

Val Asn Asn Ala Tyr Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val  
485 490 495

Phe Ser Gly Thr Ser Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr  
500 505 510

Pro Lys Glu Val His Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu  
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Tyr Lys Ser Arg Pro Thr His Ala His Pro Leu Phe Tyr Gly Leu Val  
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Lys Thr Ala Leu Glu Leu Arg Val His Pro  
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<211> 3462

**<212> DNA**

<213> *Corynebacterium glutamicum*

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<222> (101) .. (3439)

<223> RXN02234

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Met Pro Lys Arg Ser  
1 5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163  
Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly  
10 15 20

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211  
Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu  
25 30 35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259  
Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr  
40 45 50

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307  
Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile  
55 60 65

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc 355  
Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly  
70 75 80 85

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403  
 His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu  
 90 95 100

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 Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly  
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 Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp  
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cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547  
 Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala  
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 Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala  
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gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc 643  
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 170 175 180

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691  
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 185 190 195

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa 739  
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 Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr  
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gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835  
 Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu  
 230 235 240 245

ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883  
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu  
 250 255 260

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931  
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile  
 265 270 275

cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc 979  
 Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile  
 280 285 290

aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg  
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 Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val  
 295 300 305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc  
 1075  
 Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala  
 310 315 320 325

aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc  
 1123  
 Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr  
 330 335 340

aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac  
 1171  
 Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp  
 345 350 355

tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc  
 1219  
 Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly  
 360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg  
 1267  
 Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met  
 375 380 385

tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc  
 1315  
 Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser  
 390 395 400 405

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 1363  
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 410 415 420

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 1411  
 Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys  
 425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt  
 1459  
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu  
 440 445 450

ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg  
 1507  
 Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp  
 455 460 465

ttc ctc gcc gag ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt  
 1555  
 Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val  
 470 475 480 485

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 1603  
 Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met  
 490 495 500

ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc  
 1651  
 Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly  
 505 510 515

gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta  
 1699  
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val  
 520 525 530

ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg  
1747

Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro  
535 540 545

tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc  
1795

Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val  
550 555 560 565

gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca  
1843

Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro  
570 575 580

aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca  
1891

Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala  
585 590 595

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1939

Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys  
600 605 610

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac  
1987

Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr  
615 620 625

ttc gag cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag  
2035

Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu  
630 635 640 645

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2083

Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln  
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2131

Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val  
665 670 675

att ggt acc tcc cca gag gca atc gac atg gct gag gac cgt ggc gag  
2179

Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu  
680 685 690

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2227

Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly  
695 700 705

acc gca acc tct ttc gaa gag gct cgc aca gta gcc gat gag atc agc  
2275

Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser  
710 715 720 725

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 2323  
 Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met  
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gag att gtc tac gat gag gct tcc ctc gag gat tac atc aac cgc gca  
 2371  
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 745 750 755

act gag ttg tct tct gac cac cca gtg ctg gtt gac cgc ttc cta gac  
 2419  
 Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp  
 760 765 770

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 2467  
 Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val  
 775 780 785

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 2515  
 Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser  
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 2563  
 Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp  
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gta cag ggc ctg atg aac gtc cag tac gca ctc aag gac gac atc ctc  
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 2755  
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 870 875 880 885

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2899

Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr  
920 925 930

ctg gac acc ctg ctt tcc cca gag atg aag tcc act ggc gag gtc atg  
2947

Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met  
935 940 945

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2995

Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly  
950 955 960 965

gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct  
3043

Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala  
970 975 980

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3091

Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu  
985 990 995

atg ggc tac aag atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc  
3139

Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg  
1000 1005 1010

cgc aac ggc att gag tgt gaa gtt gtg ctc aag gct tcc gac atc cgc  
3187

Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg  
1015 1020 1025

gaa ggt gta gag ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa  
3235

Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu  
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gtt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac  
3283

Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His  
1050 1055 1060

gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg  
3331

Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu  
1065 1070 1075

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3379

Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala  
1080 1085 1090

ctg cgt gag ggc gtt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac  
3427

Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His  
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<210> 1000

<211> 1113

<212> PRT

<213> Corynebacterium glutamicum

<400> 1000

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 Ala Cys Arg Val Leu Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn  
 35 40 45  
 Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr  
 50 55 60  
 Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys  
 65 70 75 80  
 Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly  
 85 90 95  
 Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile  
 100 105 110  
 Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile  
 115 120 125  
 Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile  
 130 135 140  
 Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu Val  
 145 150 155 160  
 His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser  
 165 170 175  
 Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp  
 180 185 190  
 Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn  
 195 200 205  
 Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu  
 210 215 220  
 Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu  
 225 230 235 240  
 Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala  
 245 250 255  
 Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln

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Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	Asn	
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Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	Glu	
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Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	Thr	
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Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	Thr	
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Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala	Phe	
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Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala	Phe	
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Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys	Ser	
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Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu	Asn	
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Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr	Lys	
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Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala	Val	
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Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val	Glu	
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Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala	Ser	
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Ser	Ile	Asp	Pro	Trp	Phe	Leu	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gln	Phe	
465					470					475					480	
Arg	Gln	Lys	Leu	Val	Asp	Ala	Pro	Phe	Leu	Asn	Glu	Asp	Leu	Leu	Arg	
485					490					495						
Glu	Ala	Lys	Phe	Met	Gly	Leu	Ser	Asp	Leu	Gln	Ile	Ala	Ala	Leu	Arg	
500					505					510						
Pro	Glu	Phe	Ala	Gly	Glu	Asp	Gly	Val	Arg	Thr	Leu	Arg	Leu	Ser	Leu	
515					520					525						
Gly	Ile	Arg	Pro	Val	Phe	Lys	Thr	Val	Asp	Thr	Cys	Ala	Ala	Glu	Phe	
530					535					540						
Glu	Ala	Lys	Thr	Pro	Tyr	His	Tyr	Ser	Ala	Tyr	Glu	Leu	Asp	Pro	Ala	
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Leu	Gly	Ser	Gly	Pro	Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp	Tyr	
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Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr  
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 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr  
 610 615 620  
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu  
 625 630 635 640  
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val  
 645 650 655  
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys  
 660 665 670  
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala  
 675 680 685  
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro  
 690 695 700  
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val  
 705 710 715 720  
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu  
 725 730 735  
 Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp  
 740 745 750  
 Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu Val  
 755 760 765  
 Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys  
 770 775 780  
 Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu  
 785 790 795 800  
 Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr  
 805 810 815  
 Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu  
 820 825 830  
 Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu  
 835 840 845  
 Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg  
 850 855 860  
 Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala  
 865 870 875 880  
 Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu  
 885 890 895  
 Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala  
 900 905 910



Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg  
 915 920 925  
 Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser  
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 Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala  
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 Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val  
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 Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr  
 995 1000 1005  
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&lt;222&gt; (1)..(3198)

&lt;223&gt; FRXA02234

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acc tac gtg gag cca atc gag ccg gaa tac atc gac aag att ttc gct 96  
 Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala  
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 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu

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gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro 115 120 125			384
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gac ctt gag cgc atc gct ggt ggc gga ctt gct gca tct cct gaa gca Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala 145 150 155 160			480
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gag atg aac cca cgt gtg tct cgt tcc tcc gct ctg gca tcc aag gca Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala 260 265 270			816
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 1872  
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 1920  
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 625 630 635 640  
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 1968  
 Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu  
 645 650 655  
 cct gct cca gca ttc ggc acc gca acc tct ttc gaa gag gct cgc aca  
 2016  
 Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr  
 660 665 670  
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 Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val

675	680	685
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Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu 705 710 715 720		
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Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu 725 730 735		
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Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu 740 745 750		
gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg 2304		
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met 755 760 765		
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Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys 770 775 780		
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Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala 785 790 795 800		
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cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag 2496		
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys 820 825 830		
gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat 2544		
Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp 835 840 845		
gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac 2592		
Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp 850 855 860		
gct cca atc gct gtg aag gaa gca gtg ttg ccg ttc aac cgc ttc cgt 2640		
Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg 865 870 875 880		

cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag  
2688

Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys  
885 890 895

tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat  
2736

Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr  
900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc  
2784

Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr  
915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca  
2832

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc  
2880

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
945 950 955 960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc  
2928

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat  
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt  
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg  
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val  
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct  
3120

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg  
3168

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala  
1045 1050 1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc  
3218

Leu Gln Glu Leu Asp His Ala Val Lys Ala  
1060 1065

gag  
3221

<210> 1002

<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 1002

Gly Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His  
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Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala  
20 25 30

Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu  
35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly  
50 55 60

Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala  
65 70 75 80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr  
85 90 95

Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu  
100 105 110

Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro  
115 120 125

Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu  
130 135 140

Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala  
145 150 155 160

Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu  
165 170 175

Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile  
180 185 190

Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val  
195 200 205

Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp  
210 215 220

Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys  
225 230 235 240

Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile  
245 250 255

Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala  
260 265 270

Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr  
 275 280 285  
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala  
 290 295 300  
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala  
 305 310 315 320  
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys  
 325 330 335  
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu  
 340 345 350  
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr  
 355 360 365  
 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala  
 370 375 380  
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val  
 385 390 395 400  
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala  
 405 410 415  
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln  
 420 425 430  
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu  
 435 440 445  
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu  
 450 455 460  
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser  
 465 470 475 480  
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu  
 485 490 495  
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro  
 500 505 510  
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu  
 515 520 525  
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp  
 530 535 540  
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu  
 545 550 555 560  
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp  
 565 570 575  
 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met  
 580 585 590  
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile



595	600	605
Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys 610 615 620		
Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met 625 630 635 640		
Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu 645 650 655		
Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr 660 665 670		
Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val 675 680 685		
Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu 690 695 700		
Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu 705 710 715 720		
Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu 725 730 735		
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu 740 745 750		
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met 755 760 765		
Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys 770 775 780		
Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala 785 790 795 800		
Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser 805 810 815		
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys 820 825 830		
Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp 835 840 845		
Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp 850 855 860		
Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg 865 870 875 880		
Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys 885 890 895		
Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr 900 905 910		
Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr 915 920 925		

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
 930 935 940

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
 945 950 955 960

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
 965 970 975

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
 980 985 990

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
 995 1000 1005

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val  
 1010 1015 1020

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
 1025 1030 1035 1040

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala  
 1045 1050 1055

Leu Gln Glu Leu Asp His Ala Val Lys Ala  
 1060 1065

<210> 1003  
 <211> 424  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(424)  
 <223> RXN00450

<400> 1003  
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gttttgataa tgatctggct cgggtgggtgg gattcgacta gtg ggc gtt tta cct 115  
 Val Gly Val Leu Pro  
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu  
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211  
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val  
 25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259  
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg  
 40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307  
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg  
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr  
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403  
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val  
 90 95 100

ggt gct cga atc gga cgc atc 424  
 Gly Ala Arg Ile Gly Arg Ile  
 105

<210> 1004

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1004

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg  
 1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile  
 100 105

<210> 1005

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1005

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115  
 Val Gly Val Leu Pro  
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu

	10	15	20	
gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc				211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val				
	25	30	35	
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga				259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg				
	40	45	50	
gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga				307
Glu Ala Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg				
	55	60	65	
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc				355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr				
	70	75	80	85
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg				403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val				
	90	95	100	
ggt gct cga atc gga				418
Gly Ala Arg Ile Gly				
	105			

&lt;210&gt; 1006

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1006

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg			
1	5	10	15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val			
20	25	30	

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr			
35	40	45	

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu			
50	55	60	

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg			
65	70	75	80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys			
85	90	95	

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly	
100	105

&lt;210&gt; 1007

&lt;211&gt; 1368

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1345)

&lt;223&gt; RXN02272

&lt;400&gt; 1007

tattttaactc cacactaata cctgtcaagc aatagaatag atagcatctg gatcctccag 60

agtttgaaaa tatgccttga catgtagaaa tggagttctt gtg cgc att aca aac 115  
 Val Arg Ile Thr Asn  
 1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163  
 Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly  
 10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211  
 Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp  
 25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259  
 His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln  
 40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307  
 Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile  
 55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg 355  
 Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp  
 70 75 80 85

gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg 403  
 Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala  
 90 95 100

aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc 451  
 Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe  
 105 110 115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499  
 Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu  
 120 125 130

gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag 547  
 Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln  
 135 140 145

att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag 595  
 Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln  
 150 155 160 165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc 643  
 Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly  
 170 175 180

atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa 691  
 Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys  
 185 190 195

tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac 739  
 Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His

200	205	210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc			787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala			
215	220	225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat			835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His			
230	235	240	245
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta			883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu			
250	255	260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa			931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu			
265	270	275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt			979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly			
280	285	290	
gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt			
1027			
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe			
295	300	305	
tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat			
1075			
Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp			
310	315	320	325
cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca			
1123			
Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr			
330	335	340	
gcc agc cac ttg aag aat gca cta tgc ttc atc acc acc aat cca gcc			
1171			
Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala			
345	350	355	
gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg			
1219			
Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala			
360	365	370	
aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga			
1267			
Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg			
375	380	385	
aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc			
1315			
Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser			
390	395	400	405
agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc			
1365			
Arg Glu Pro Glu Gln Val Asp Trp Asn Ile			
410	415		

ctt  
1368

<210> 1008

<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 1008

Val Arg Ile Thr Asn Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp  
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Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile  
20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg  
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala  
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu  
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys  
85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu  
100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr  
115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu  
130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala  
145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala  
165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly  
180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala  
195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe  
210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln  
225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr  
245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala  
260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly  
275 280 285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly  
290 295 300

Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro  
305 310 315 320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val  
325 330 335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile  
340 345 350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala  
355 360 365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys  
370 375 380

Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly  
385 390 395 400

Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile  
405 410 415

<210> 1009

<211> 1368

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1345)

<223> FRXA02272

<400> 1009

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agtttgaaaa tatgccttga catgtagaaa tggagttctt gtg cgc att aca aac 115  
Val Arg Ile Thr Asn  
1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163  
Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly  
10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211  
Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp  
25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259  
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln  
40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307  
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile  
55 60 65



cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg	355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp	
70 75 80 85	
gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg	403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala	
90 95 100	
aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc	451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe	
105 110 115	
atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa	499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu	
120 125 130	
gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag	547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln	
135 140 145	
att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag	595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln	
150 155 160 165	
aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc	643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly	
170 175 180	
atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa	691
Ile Pro His Leu Glu Pro Thr Arg Asp Gly Val Glu Ser Val Lys	
185 190 195	
tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac	739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His	
200 205 210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala	
215 220 225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat	835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His	
230 235 240 245	
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta	883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu	
250 255 260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa	931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu	
265 270 275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt	979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly	
280 285 290	
gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt	
1027	
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe	
295 300 305	

tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat  
1075

Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp  
310 315 320 325

cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca  
1123

Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr  
330 335 340

gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc  
1171

Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala  
345 350 355

gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg  
1219

Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala  
360 365 370

aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga  
1267

Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg  
375 380 385

aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc  
1315

Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser  
390 395 400 405

agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc  
1365

Arg Glu Pro Glu Gln Val Asp Trp Asn Ile  
410 415

ctt  
1368

<210> 1010

<211> 415

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1010

Val Arg Ile Thr Asn Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp  
1 5 10 15

Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile  
20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg  
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala  
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu  
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys  
 85 90 95  
 Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu  
 100 105 110  
 His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr  
 115 120 125  
 Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu  
 130 135 140  
 Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala  
 145 150 155 160  
 Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala  
 165 170 175  
 Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly  
 180 185 190  
 Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala  
 195 200 205  
 Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe  
 210 215 220  
 Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln  
 225 230 235 240  
 Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr  
 245 250 255  
 Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala  
 260 265 270  
 Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly  
 275 280 285  
 Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly  
 290 295 300  
 Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro  
 305 310 315 320  
 Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val  
 325 330 335  
 Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile  
 340 345 350  
 Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala  
 355 360 365  
 Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys  
 370 375 380  
 Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly  
 385 390 395 400  
 Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile

405

410

415

&lt;210&gt; 1011

&lt;211&gt; 580

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; RXN03004

&lt;400&gt; 1011

gctagcacga taaaaatcag cgccagcacc acgcgccccca ggaacctcat cgcagcaacc 60

cgtggcccaa ccctgaacgc tgaacgctac actggttgac gtg ctt ctt tca gat 115  
 Val Leu Leu Ser Asp  
 1 5

cgt gac att cgt aaa tca att gac gca ggc gac ttg gga att gaa cct 163  
 Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp Leu Gly Ile Glu Pro  
 10 15 20

ttc gac gct gag ctg att cag ccg tgc agt gtc gat gtc cgc atg gac 211  
 Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val Asp Val Arg Met Asp  
 25 30 35

cgc tac ttc cgg gtt ttc aat aac tct aag tac acc cac att gac cct 259  
 Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr Thr His Ile Asp Pro  
 40 45 50

aag ttg aat cag gat gag ctg acc agc ctt gtt gag gtt gag gac ggc 307  
 Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val Glu Val Glu Asp Gly  
 55 60 65

gag ggc ttt gtg ctg cat ccg ggt gag ttt gtg ctg gcg tcc acg ctg 355  
 Glu Gly Phe Val Leu His Pro Gly Glu Phe Val Leu Ala Ser Thr Leu  
 70 75 80 85

gaa aag ttc act ttg cct gcg cat ctg gct ggt cgt ttg gag ggt aag 403  
 Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly Arg Leu Glu Gly Lys  
 90 95 100

tgc tct ctt ggt cgt ctt ggc ttg ttg acg cac tct act gct ggt ttc 451  
 Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His Ser Thr Ala Gly Phe  
 105 110 115

att gat cct ggt ttt agt ggt tac atc acg ttg gag ttg tcc aat gtg 499  
 Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu Glu Leu Ser Asn Val  
 120 125 130

gct aat ctg ccg atc acg ttg tgg ccg ggt atg aag gtg ggg cag ctg 547  
 Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met Lys Val Gly Gln Leu  
 135 140 145

gct ttg ttc cag atg agt tcc cct gcg gag act 580  
 Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr  
 150 155 160

<210> 1012  
 <211> 160  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1012  
 Val Leu Leu Ser Asp Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp  
     1                    5                    10                    15  
 Leu Gly Ile Glu Pro Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val  
                     20                    25                    30  
 Asp Val Arg Met Asp Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr  
             35                    40                    45  
 Thr His Ile Asp Pro Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val  
     50                    55                    60  
 Glu Val Glu Asp Gly Glu Gly Phe Val Leu His Pro Gly Glu Phe Val  
     65                    70                    75                    80  
 Leu Ala Ser Thr Leu Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly  
                     85                    90                    95  
 Arg Leu Glu Gly Lys Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His  
             100                    105                    110  
 Ser Thr Ala Gly Phe Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu  
             115                    120                    125  
 Glu Leu Ser Asn Val Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met  
     130                    135                    140  
 Lys Val Gly Gln Leu Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr  
     145                    150                    155                    160

<210> 1013  
 <211> 225  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(202)  
 <223> RXN03137

<400> 1013  
 cggcgagttc atttggactg gcggcgactg ccacatttat gacaaccaca aggaacaggt 60  
 cgcgaggacag ctgagccgat aagctcgccc ctaccccacc ttg gag ctc aac aag 115  
   Leu Glu Leu Asn Lys  
   1                    5  
 gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc 163  
 Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly  
                     10                    15                    20

tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcgggtgc 212  
 Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val Ala Val  
                   25                                  30

gatttgaggca caa 225

<210> 1014

<211> 34

<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

Leu Glu Leu Asn Lys Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp  
   1                  5                                  10                                  15

Ile Thr Val Ser Gly Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val  
                   20                                  25                                  30

Ala Val

<210> 1015

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXN03171

<400> 1015

atacttttggtt ggactggaaa agtggccggtt tggttccctc caagcccaaa ttcgcccgcg 60

cggctcttctt ctgggaggca atgatttaac atgtgaagct atg gac atc acc atc 115  
   Met Asp Ile Thr Ile  
   1                                  5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
                   10                                  15                                  20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
                   25                                  30                                  35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
                   40                                  45                                  50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
                   55                                  60                                  65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
                   70                                  75                                  80                                  85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403

Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
                             90                            95                            100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
                             105                            110                            115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
                             120                            125                            130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
                             135                            140                            145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
                             150                            155                            160                            165

gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
                             170

<210> 1016  
 <211> 171  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1016  
 Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr  
           1                            5                            10                            15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
                             20                            25                            30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
                             35                            40                            45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
                             50                            55                            60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
                             65                            70                            75                            80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
                             85                            90                            95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
                             100                            105                            110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
                             115                            120                            125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
                             130                            135                            140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
                             145                            150                            155                            160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser

165

170

<210> 1017  
 <211> 613  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(613)  
 <223> FRXA02857

&lt;400&gt; 1017

atactttgtt ggactggaaa agtggccgtt tggttccctc caagcccaaa ttcgcccgcg 60

cggtcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115  
 Met Asp Ile Thr Ile  
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165

gac gca ttg gcg gaa tct 613



Asp Ala Leu Ala Glu Ser  
170

<210> 1018

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1018

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr  
1 5 10 15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser  
165 170

<210> 1019

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXA02771

<400> 1019

gtttgtgata gatcgacag tcggtaacgt tgttgtaaat acagacctag ccggtatcgg 60

atggaacatg gaccgttggc ccagaagtga ggaataagta gtg agc gaa caa gct 115  
Val Ser Glu Gln Ala  
1 5

cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163  
 Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu Asp Lys Lys Thr Arg  
                   10                  15                  20

tat gtg cag gat ttc cca gaa aaa ggt gtg ctt ttt gaa gac ctc acc 211  
 Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr  
                   25                  30                  35

ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259  
 Pro Val Leu Glu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met  
                   40                  45                  50

gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307  
 Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp  
                   55                  60                  65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355  
 Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu  
                   70                  75                  80                  85

ggt gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403  
 Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val  
                   90                  95                  100

acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451  
 Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro  
                   105                  110                  115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499  
 Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp  
                   120                  125                  130

gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547  
 Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu  
                   135                  140                  145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595  
 Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro  
                   150                  155                  160                  165

ggc ctc ggc ggt agg gat aat ctt ggt gat agg ccc gtc att gtg gtc 643  
 Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg Pro Val Ile Val Val  
                   170                  175                  180

aga gat cct cag tagaaggatc gaaagaaagg cgg 678  
 Arg Asp Pro Gln  
                   185

&lt;210&gt; 1020

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1020

Val Ser Glu Gln Ala Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu  
   1                  5                  10                  15

Asp Lys Lys Thr Arg Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu  
                   20                  25                  30

Phe Glu Asp Leu Thr Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala  
35 40 45

Val Val Asp Ala Met Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile  
50 55 60

Ile Gly Gly Leu Asp Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala  
65 70 75 80

Tyr Lys Leu Gly Leu Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu  
85 90 95

Pro Pro Pro Val Val Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala  
100 105 110

Ala Leu Glu Leu Pro Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile  
115 120 125

Val Leu Ile Asp Asp Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala  
130 135 140

Arg Lys Leu Ile Glu Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu  
145 150 155 160

Ala Ile Glu Val Pro Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg  
165 170 175

Pro Val Ile Val Val Arg Asp Pro Gln  
180 185

<210> 1021

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXA01512

<400> 1021

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tgattgacac ctgaatctac aacacaaggg gaacgcgacg atg agc aac aac gta 115  
Met Ser Asn Asn Val  
1 5

gaa atg gcc gac cac aaa gat ctc aat gtt cca gcc aac cca tac ggc 163  
Glu Met Ala Asp His Lys Asp Leu Asn Val Pro Ala Asn Pro Tyr Gly  
10 15 20

acc gac att gaa tca gta ttg atc agc gaa gag aag ctc aag cag cgc 211  
Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu Lys Leu Lys Gln Arg  
25 30 35

atc gcc gaa atg gcc aag cgc gtc tcc gaa gag ttc aaa gac gcc gaa 259  
Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu Phe Lys Asp Ala Glu  
40 45 50

gaa gac ctc atc ctg gtg tgc gtg ctc aag ggc gcg ttc tac ttc ctg 307

Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly Ala Phe Tyr Phe Leu  
 55 60 65  
 gca gat ttc tcc cgc atg ctc gac atc ccc acc cag tcc gag ttc atg 355  
 Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr Gln Ser Glu Phe Met  
 70 75 80 85  
 gcg gtg tcc tct tac gga aac tcc acc tcc tct tca ggc gtg gtg cgc 403  
 Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser Ser Gly Val Val Arg  
 90 95 100  
 atc ctc aag gac ctg gac aag gaa att gaa ggc cgc gac gtt ttg atc 451  
 Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly Arg Asp Val Leu Ile  
 105 110 115  
 gtg gaa gac atc atc gat tcc gga ctg acc ctg tcc tgg ctg atg cgc 499  
 Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu Ser Trp Leu Met Arg  
 120 125 130  
 aac ctg aaa aac cgc aac cct aag tcc ctc aac gtg atc acc ttg ctg 547  
 Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn Val Ile Thr Leu Leu  
 135 140 145  
 cgt aag cca gag cgc ctg acc acc aac atc gac atg ttc gac att gga 595  
 Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp Met Phe Asp Ile Gly  
 150 155 160 165  
 ttt gat att cca aat gag ttt gtt gtg ggc tac gga ctt gat ttc gca 643  
 Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr Gly Leu Asp Phe Ala  
 170 175 180  
 gaa cgc tac cgc gac ctg cca tat gtg ggc acc ctc gag cct cac gtg 691  
 Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr Leu Glu Pro His Val  
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 tac tcc gac tagtaatcaa aagtgcgaaa gag 723  
 Tyr Ser Asp  
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&lt;211&gt; 200

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1022

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 Lys Leu Lys Gln Arg Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu  
 35 40 45  
 Phe Lys Asp Ala Glu Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly  
 50 55 60  
 Ala Phe Tyr Phe Leu Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr  
 65 70 75 80

Gln Ser Glu Phe Met Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser  
85 90 95

Ser Gly Val Val Arg Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly  
100 105 110

Arg Asp Val Leu Ile Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu  
115 120 125

Ser Trp Leu Met Arg Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn  
130 135 140

Val Ile Thr Leu Leu Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp  
145 150 155 160

Met Phe Asp Ile Gly Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr  
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Gly Leu Asp Phe Ala Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr  
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Leu Glu Pro His Val Tyr Ser Asp  
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Met Thr Glu Glu Arg  
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gag att ctg acc tat gag atg ttc gga aca gca atg cgg gag ctg gcc 163  
Glu Ile Leu Thr Tyr Glu Met Phe Gly Thr Ala Met Arg Glu Leu Ala  
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caa gaa att att gat gac tac cag cca gat tgc gtg ctg tcc att gcg 211  
Gln Glu Ile Ile Asp Asp Tyr Gln Pro Asp Cys Val Leu Ser Ile Ala  
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cgt ggt ggt ctt cta atc ggt ggc gca ctt ggt tat gcg ctg ggt atc 259  
Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly Tyr Ala Leu Gly Ile  
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Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr Thr Asp Ile Gly Glu  
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cac ttg gag gag cca atg atg ctg cct cca act cca aaa gct gtt gat 355  
His Leu Glu Glu Pro Met Met Leu Pro Pro Thr Pro Lys Ala Val Asp  
70 75 80 85

ctc tcg gga atg cgt gtg ctc gtc gct gac gat gtc gcg gat acc gga 403  
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aag act ctt gag ttg gtc agg gac ttc ctg ggt gac caa gtt gtc gaa 451  
 Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly Asp Gln Val Val Glu  
                   105                  110                  115

gtg cgc act gca gtg atc tat cac aag cca aac agt gtg ttt aag ccg 499  
 Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn Ser Val Phe Lys Pro  
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gag tat gtg tgg cgt gag act gat aag tgg att aac ttc cca tgg tct 547  
 Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile Asn Phe Pro Trp Ser  
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<213> Corynebacterium glutamicum

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                   20                  25                  30

Val Leu Ser Ile Ala Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly  
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Tyr Ala Leu Gly Ile Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr  
           50                  55                  60

Thr Asp Ile Gly Glu His Leu Glu Glu Pro Met Met Leu Pro Pro Thr  
           65                  70                  75                  80

Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp  
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Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly  
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Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn  
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Ser Val Phe Lys Pro Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile  
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Pro	Ala	Pro	Glu	Asn	Leu	Leu	Asp	Ala	Glu	Arg	Ile	Gln	Met	Ile	Lys	
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Asn	Phe	Arg	Asn	Glu	Leu	Thr	Gly	Phe	Met	Leu	Asn	Tyr	Gln	Phe	Gly	
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Ile	Asp	Glu	Ile	Leu	Thr	Lys	Ile	Asn	Ile	Leu	Lys	Thr	Glu	Phe	Ser	
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cag	ctg	cac	gaa	tac	gca	cct	atc	gag	cac	gta	tct	tca	cga	ttg	aag	307
Gln	Leu	His	Glu	Tyr	Ala	Pro	Ile	Glu	His	Val	Ser	Ser	Arg	Leu	Lys	
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Ser	Leu	Ala	Ala	Ile	Lys	Asp	Thr	Val	Phe	Asp	Ile	Ala	Gly	Ile	Arg	
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Asn	Pro	Lys	Pro	Asn	Gly	Tyr	Lys	Ser	Leu	His	Leu	Ile	Leu	Gln	Val	
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Pro	Val	Phe	Leu	Ser	Asn	Ser	Val	Glu	Lys	Val	Asn	Val	Glu	Val	Gln	
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Ile	Arg	Thr	Ile	Ala	Met	Asp	Phe	Trp	Ala	Ser	Leu	Glu	His	Lys	Ile	
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 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu  
                   185                                  190                                  195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740  
 Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr  
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<213> Corynebacterium glutamicum

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Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu  
                   35                                  40                                  45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val  
                   50                                  55                                  60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg  
       65                                  70                                  75                                  80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp  
                   85                                  90                                  95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala  
                   100                                  105                                  110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala  
                   115                                  120                                  125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His  
                   130                                  135                                  140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val  
       145                                  150                                  155                                  160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser  
                   165                                  170                                  175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser  
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Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu  
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Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
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Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
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Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
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Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
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Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
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aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 643
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
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ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 691

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 Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu  
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 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val  
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cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 835  
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu  
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att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 883  
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gaa gtg ctt ggt cga cca aag cac tac tgg tct atc tat caa aag atg 931  
 Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser Ile Tyr Gln Lys Met  
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 295 300 305

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Lys	Val	Ala	Asp	Arg	Leu	His	Asn	Met	Arg	Thr	Met	Arg	Phe	Leu	Pro	
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Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg  
 35 40 45

Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His  
 50 55 60

Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr  
 65 70 75 80

Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr  
 85 90 95

Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu  
 100 105 110

Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala  
 115 120 125

Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro  
 130 135 140

Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr  
 145 150 155 160

Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr  
 165 170 175

Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val  
 180 185 190  
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys  
 195 200 205  
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp  
 210 215 220  
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu  
 225 230 235 240  
 Asn Asn Ile Ala Ala Glu Val Leu Gly Arg Pro Lys His Ser Gly Leu  
 245 250 255  
 Ser Phe Lys Arg  
 260

<210> 1031  
 <211> 262  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(262)  
 <223> FRXA02773

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 Met Ile Val Arg Gly  
 1 5  
 cgt gat ttt gac gat att ttt gat ctt gtt ggc atc cgc ntc ctg gna 163  
 Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile Arg Xaa Leu Xaa  
 10 15 20  
 gac aac gtg aac aac tgg gta cgc cgc cnt cgg tgt cgt gca ctc ccn 211  
 Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg Cys Arg Ala Leu Pro  
 25 30 35  
 gtn caa tgc tct gnc tgg ncg ntt caa aga cta tat ttc agc ccc gcg 259  
 Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu Tyr Phe Ser Pro Ala  
 40 45 50  
 ctt 262  
 Leu

<210> 1032  
 <211> 54  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1032  
 Met Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly  
 1 5 10 15

Ile Arg Xaa Leu Xaa Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg  
 20 25 30

Cys Arg Ala Leu Pro Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu  
 35 40 45

Tyr Phe Ser Pro Ala Leu  
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<210> 1033

<211> 654

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(631)

<223> RXA01835

<400> 1033

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ttctctgcgtg aatacacttt ccccgcgct tcgcaaagct atg aat act gcc gcg 115  
 Met Asn Thr Ala Ala  
 1 5

tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163  
 Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val  
 10 15 20

agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211  
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp  
 25 30 35

gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259  
 Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val  
 40 45 50

ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307  
 Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg  
 55 60 65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355  
 Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp  
 70 75 80 85

aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403  
 Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser  
 90 95 100

tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451  
 Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met  
 105 110 115

tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499  
 Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg  
 120 125 130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547

Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr  
 135 140 145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595  
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu  
 150 155 160 165

ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641  
 Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala  
 170 175

gcggcgctcga taa 654

<210> 1034  
 <211> 177  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1034  
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 1 5 10 15

Gly Ile Pro Tyr Val Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala  
 20 25 30

Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp  
 35 40 45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala  
 50 55 60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln  
 65 70 75 80

Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu  
 85 90 95

Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys  
 100 105 110

Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu  
 115 120 125

Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp  
 130 135 140

Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu  
 145 150 155 160

Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser  
 165 170 175

Ala

<210> 1035  
 <211> 1395  
 <212> DNA  
 <213> Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1372)

&lt;223&gt; RXA01483

&lt;400&gt; 1035

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gcgtgcacgc catgagcaac ttcggagggt gaaaaagtag atg tac ccc tat tcc 115
                               Met Tyr Pro Tyr Ser
                               1                     5

gac gca gac gct ttt cga cgc cag cct gag cgc gcc aag tcc agc caa 163
Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg Ala Lys Ser Ser Gln
                      10                      15                      20

ctg cgt acc agc gcc gta gac acc cgc agc gcg ttc gcc cgc gac cgg 211
Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala Phe Ala Arg Asp Arg
                      25                      30                      35

gct cgc gtg ctg cat tct gct gct ctt cga cgc ctc gcg gat aaa acc 259
Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg Leu Ala Asp Lys Thr
                      40                      45                      50

caa gtg gtt ggc ccc aat gat ggt gat act ccg cgc acc cgg ctg acg 307
Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro Arg Thr Arg Leu Thr
                      55                      60                      65

cac tct ttg gaa gta gct caa att gca cgg gga atc gga gct gga ctg 355
His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly Ile Gly Ala Gly Leu
                      70                      75                      80                      85

gat ttg gat cct gat ctg tgc gat ctg gca ggg ctg tgc cat gac att 403
Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly Leu Cys His Asp Ile
                      90                      95                      100

ggg cat ccg ccg tat gga cac aac ggt gaa aac gcg ttg aat gaa gtt 451
Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn Ala Leu Asn Glu Val
                      105                      110                      115

gct gcg gcc tgt gga gga ttt gag ggc aac gcc caa acc ttg cgt att 499
Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala Gln Thr Leu Arg Ile
                      120                      125                      130

ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt 547
Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe
                      135                      140                      145

ggg ctg aac ttg tcg cgg gct gct ctt gat gct gca tgt aag tat ccg 595
Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala Ala Cys Lys Tyr Pro
                      150                      155                      160                      165

tgg gct aaa aca aat gcg gat ggc agt gtc aat aag aaa tac agt gct 643
Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala
                      170                      175                      180

tat gac gag gac gca gaa atc ctc gct tgg att aga caa ggc cat gag 691
Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu
                      185                      190                      195

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gat ctt cgc cca ccg atc gaa gcg cag gtc atg gac ttt tct gat gac 739  
 Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met Asp Phe Ser Asp Asp  
 200 205 210

att gcc tac tcg gtg cac gat gtg gaa gac ggt att gta tcc ggg cgt 787  
 Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg  
 215 220 225

atc gac tta aaa gtg ctg tgg gac ctg gtt gaa tta gca gct ttg gca 835  
 Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala  
 230 235 240 245

gac aaa gga gca gct gct ttc gga ggt tcg cct gca gag ctc atc gag 883  
 Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu  
 250 255 260

ggt gca gca tcg ttg cgg gaa ctt ccg gtg gtg gct gcc gct gcg gat 931  
 Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Asp  
 265 270 275

ttt gat ttc tca ctg cgt tcc tac gct gcg ctg aag gcg atg act tca 979  
 Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser  
 280 285 290

gaa cta gtg gga aga tac gtt ggc tct acc atc gag tca aca aag aaa  
 1027  
 Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys  
 295 300 305

aca cac gct ggc att gat gtg gga cgc atg cac ggc gat ttg atc att  
 1075  
 Thr His Ala Gly Ile Asp Val Gly Arg Met His Gly Asp Leu Ile Ile  
 310 315 320 325

cca gaa aca gcg gcc agt gaa gta aaa ctg ctc aaa acg tta gcg gtt  
 1123  
 Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu Lys Thr Leu Ala Val  
 330 335 340

ctc tac gtg atg gat gac cca ggg cac ctt gcg cgc caa aac agg caa  
 1171  
 Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala Arg Gln Asn Arg Gln  
 345 350 355

cgg gat cgt atc ttc cgg gtt ttt gac tac ctg gtg ctg ggg gct ccg  
 1219  
 Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu Val Leu Gly Ala Pro  
 360 365 370

gga tcg ttg gat ccg atg tat cgc cag tgg ttt att gaa gcg gat tca  
 1267  
 Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe Ile Glu Ala Asp Ser  
 375 380 385

gaa tcg gaa cag atc cgt gtg att gtt gat cag att gcg tcg atg acg  
 1315  
 Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr  
 390 395 400 405

gag tct cgt ctg gaa cgc ctt gcc cgg aat gct gct gac atc tca gga  
 1363

Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala Ala Asp Ile Ser Gly  
 410 415 420

ttt ttg gga taattgggta gagcagcagt aag  
 1395  
 Phe Leu Gly

&lt;210&gt; 1036

&lt;211&gt; 424

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1036

Met Tyr Pro Tyr Ser Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg  
 1 5 10 15

Ala Lys Ser Ser Gln Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala  
 20 25 30

Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg  
 35 40 45

Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro  
 50 55 60

Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly  
 65 70 75 80

Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly  
 85 90 95

Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn  
 100 105 110

Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala  
 115 120 125

Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp  
 130 135 140

Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala  
 145 150 155 160

Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn  
 165 170 175

Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile  
 180 185 190

Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met  
 195 200 205

Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly  
 210 215 220

Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu  
 225 230 235 240

Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro

245	250	255
Ala Glu Leu Ile Glu Gly Ala Ala	Ser Leu Arg Glu Leu Pro Val Val	
260	265	270
Ala Ala Ala Ala Asp Phe Asp Phe	Ser Leu Arg Ser Tyr Ala Ala Leu	
275	280	285
Lys Ala Met Thr Ser Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile		
290	295	300
Glu Ser Thr Lys Lys Thr His Ala Gly Ile Asp Val Gly Arg Met His		
305	310	315
Gly Asp Leu Ile Ile Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu		
325	330	335
Lys Thr Leu Ala Val Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala		
340	345	350
Arg Gln Asn Arg Gln Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu		
355	360	365
Val Leu Gly Ala Pro Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe		
370	375	380
Ile Glu Ala Asp Ser Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln		
385	390	395
Ile Ala Ser Met Thr Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala		
405	410	415
Ala Asp Ile Ser Gly Phe Leu Gly		
420		

&lt;210&gt; 1037

&lt;211&gt; 1131

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1108)

&lt;223&gt; RXN01027

&lt;400&gt; 1037

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gaactgtgtg caccacaacg cggaagggtga atcgcaccca	atg gca aat aag aac	115
	Met Ala Asn Lys Asn	
	1 5	

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc	163
Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile	
10 15 20	

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc	211
Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr	
25 30 35	

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc	259
Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr	
40 45 50	
aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat	307
Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp	
55 60 65	
gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg	355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro	
70 75 80 85	
aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt	403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg	
90 95 100	
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc	451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr	
105 110 115	
aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc	499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val	
120 125 130	
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca	547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala	
135 140 145	
tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca	595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala	
150 155 160 165	
gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc	643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg	
170 175 180	
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag	691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys	
185 190 195	
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc	739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro	
200 205 210	
atg ttg ttg ccc ttc aaa ccc acc gca att tac tcg gcg gtg ccc gat	787
Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr Ser Ala Val Pro Asp	
215 220 225	
cgc tgc caa gcc acc gcg ctc ccc ctt gcc gat gag ctc ggc ctc gac	835
Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp	
230 235 240 245	
gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc	883
Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro	
250 255 260	
gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg	931
Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val	
265 270 275	
ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg	979

Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp  
 280 285 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa  
 1027

Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys  
 295 300 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc  
 1075

Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly  
 310 315 320 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg ttttaaggcct  
 1128

Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 330 335

cca  
 1131

<210> 1038

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 1038

Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp  
 1 5 10 15

Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro  
 20 25 30

Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp  
 35 40 45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His  
 50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro  
 65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr  
 85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro  
 100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu  
 115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu  
 130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu  
 145 150 155 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg  
 165 170 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly  
 180 185 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala  
 195 200 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr  
 210 215 220

Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp  
 225 230 235 240

Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala  
 245 250 255

Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val  
 260 265 270

Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro  
 275 280 285

Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu  
 290 295 300

Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp  
 305 310 315 320

Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 325 330 335

&lt;210&gt; 1039

&lt;211&gt; 757

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(757)

&lt;223&gt; FRXA01024

&lt;400&gt; 1039

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gaactgtgtg caccacaacg cggaaggtga atcgcaccca atg gca aat aag aac 115  
 Met Ala Asn Lys Asn  
 1 5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163  
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile  
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211  
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr  
 25 30 35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259  
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr

40	45	50	
aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat			307
Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp			
55	60	65	
gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg			355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro			
70	75	80	85
aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt			403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg			
	90	95	100
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc			451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr			
	105	110	115
aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc			499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val			
	120	125	130
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca			547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala			
	135	140	145
tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca			595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala			
	150	155	160
gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc			643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg			
	170	175	180
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag			691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys			
	185	190	195
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc			739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro			
	200	205	210
atg ttg ttg ccc ttc aaa			757
Met Leu Leu Pro Phe Lys			
215			
<210> 1040			
<211> 219			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1040			
Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp			
1	5	10	15
Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro			
20	25	30	
Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp			
35	40	45	



Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His  
 50 55 60  
 Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro  
 65 70 75 80  
 Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr  
 85 90 95  
 Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro  
 100 105 110  
 Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu  
 115 120 125  
 Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu  
 130 135 140  
 Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu  
 145 150 155 160  
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg  
 165 170 175  
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly  
 180 185 190  
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala  
 195 200 205  
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys  
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<210> 1041  
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 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(234)  
 <223> FRXA01027

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 Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln  
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 ggt ggc gtg ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg 96  
 Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met  
 20 25 30  
 atc aaa tgg ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc 144  
 Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile  
 35 40 45  
 aag gcg aaa aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg 192  
 Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val  
 50 55 60

ttc acc ggc gct gat tac ctg gcg agt tcc ctg ccg gtt aaa 234  
 Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
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<210> 1042

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 1042

Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln  
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Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met  
 20 25 30

Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile  
 35 40 45

Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val  
 50 55 60

Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys  
 65 70 75

<210> 1043

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

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gggtcgtagg tctccaacca ggaggcggtc caacacgagg gtg aat cag gcg tgg 115  
 Val Asn Gln Ala Trp  
 1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163  
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu  
 10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211  
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp  
 25 30 35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259  
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly  
 40 45 50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307  
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp

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aag gct gcg act gct gag.cgt gag gtg tgg gag gag acc ggc atc cac			355
Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His			
70	75	80	85
ggg gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg			403
Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser			
	90	95	100
gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat			451
Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr			
	105	110	115
gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg			499
Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala			
	120	125	130
tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag			547
Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu			
	135	140	145
cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg			595
Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu			
	150	155	160
aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaacccg			648
Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg			
	170	175	
aac			651
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Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala			
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Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg			
	35	40	45
Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val			
	50	55	60
Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu			
	65	70	75
Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp			
	85	90	95
Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His			
	100	105	110
His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu			

115	120	125
Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu		
130	135	140
Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu		
145	150	155
Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg		
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(541)  
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 Met Ser Phe Gln Leu  
 1 5

gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163  
 Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser  
 10 15 20

ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211  
 Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys  
 25 30 35

cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259  
 His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala  
 40 45 50

agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307  
 Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala  
 55 60 65

att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355  
 Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala  
 70 75 80 85

gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403  
 Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr  
 90 95 100

cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451  
 His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr  
 105 110 115

tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499

Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln  
 120 125 130

gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg 541  
 Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala  
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<210> 1046

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 1046

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Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser  
 20 25 30

Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala  
 35 40 45

Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu  
 50 55 60

His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val  
 65 70 75 80

Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe  
 85 90 95

Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln  
 100 105 110

Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu  
 115 120 125

Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser  
 130 135 140

Asn Pro Ala  
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<210> 1047

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(979)

<223> RXA01878

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atagtagaaa tctggcatcc aataggtaga ttgggatgct atg gaa gaa ccc tca 115  
 Met Glu Glu Pro Ser  
 1 5

ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag	163
Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys	
10 15 20	
ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat	211
Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp	
25 30 35	
ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac	259
Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn	
40 45 50	
gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc	307
Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala	
55 60 65	
ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt	355
Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg	
70 75 80 85	
ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt	403
Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu	
90 95 100	
gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa	451
Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln	
105 110 115	
tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac	499
Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr	
120 125 130	
aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc	547
Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr	
135 140 145	
atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg	595
Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu	
150 155 160 165	
gct gcg gat cca gga tcg aag att tat ggt gtg cct agc gtg aag gcg	643
Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala	
170 175 180	
tcc ttc tac ggt cca gtt act cgc gcc ggg tcg att ggt aag aat gtc	691
Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val	
185 190 195	
ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc	739
Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg	
200 205 210	
gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg	787
Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp	
215 220 225	
ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct	835
Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala	
230 235 240 245	

gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883  
Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu  
250 255 260

cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931  
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val  
 265 270 275

act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979  
Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys  
280 285 290

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1002

<210> 1048

**<211> 293**

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

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Ala Leu Ala Glu Lys Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln  
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Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala  
35 40 45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly  
50 55 60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val  
65 70 75 80

Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp  
85 90 95

Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala  
100 105 110

Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val  
115 120 125

Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met  
130 135 140

Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu  
145 150 155 160

Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val  
165 170 175

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser  
180 185 190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu  
195 200 205

Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr  
 210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg  
 225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala  
 245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly  
 260 265 270

Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln  
 275 280 285

Gln Lys Asp Glu Lys  
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<210> 1049  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1531)  
 <223> RXN02281

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cctataaaaag cacagtttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115  
 Val Gln Lys Asp Ser  
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211  
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355  
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg  
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403  
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn  
 90 95 100

tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg 451



Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro		
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gag	tac	att	cgc	ggc	gca	cct	tcc	gct	acc	gaa	gct	cgc	cgt	gct	ggt	499	
Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly		
		120					125				130						
gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547	
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp		
	135					140					145						
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg	595	
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro		
150				155					160						165		
ctt	ttc	cac	ttc	ggg	ccg	caa	cgc	ttc	gac	atc	gcc	tgc	gcc	cgc	atc	643	
Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile		
			170					175						180			
gag	cac	tac	acc	ggc	atc	aac	gtg	gaa	cac	gtg	cag	aag	tac	att	ctg	691	
Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu		
			185					190					195				
ttc	acc	aac	tac	gcc	atg	cac	acc	acc	gag	ttc	gtg	cat	ttt	gcc	atg	739	
Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met		
		200					205					210					
tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggt	cta	tcc	ttg	cca	787	
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro		
	215					220					225						
aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggt	acg	gaa	835	
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu		
230					235				240						245		
acc	ctt	gat	ctg	act	agc	cgt	ttc	caa	atg	cct	cgt	tac	gat	ctc	atc	883	
Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile		
			250					255						260			
acc	gaa	gcc	ggt	gac	ggt	att	acc	att	atc	aac	atc	ggt	gtg	ggc	cca	931	
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro		
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tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa	979	
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu		
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gcc	tgg	gtg	atg	atc	ggc	cac	tgt	gct	ggc	atg	gac	gcc	cgc	atg	cgc		
1027																	
Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg		
	295					300					305						
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1075																	
Ile	Gly	Asp	Leu	Ile	Leu	Gly	Asn	Ala	Tyr	Gln	Arg	Glu	Asp	His	Ile		
310					315					320					325		
ctg	aat	acc	cgc	atc	cca	ctt	ggt	aat	ccg	atc	ccg	gca	ata	cca	gaa		
1123																	
Leu	Asn	Thr	Arg	Ile	Pro	Leu	Gly	Asn	Pro	Ile	Pro	Ala	Ile	Pro	Glu		
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atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac  
1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp  
345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac  
1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn  
360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc  
1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser  
375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga  
1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly  
390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg  
1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu  
410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac  
1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr  
425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa  
1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu  
440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg  
1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg  
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1545

Thr Leu Gly Glu Val Pro Phe Arg  
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<210> 1050

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala  
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val  
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
 50 55 60  
 Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
 65 70 75 80  
 Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
 85 90 95  
 Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
 100 105 110  
 Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
 115 120 125  
 Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
 130 135 140  
 Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
 145 150 155 160  
 Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
 165 170 175  
 Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
 180 185 190  
 Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
 195 200 205  
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
 210 215 220  
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
 225 230 235 240  
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
 245 250 255  
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
 260 265 270  
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
 275 280 285  
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
 290 295 300  
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
 305 310 315 320  
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
 325 330 335  
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu  
 340 345 350  
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser  
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn  
 370 375 380

Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr  
 385 390 395 400

Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu  
 405 410 415

Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln  
 420 425 430

Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala  
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Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr  
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 Val Gln Lys Asp Ser  
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gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163  
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu  
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 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn  
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aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259  
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr  
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gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307  
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly  
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 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg  
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 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn

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Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro														451
			105																										
gag	tac	att	cgc	ggc	gca	cct	tcc	gct	acc	gaa	gct	cgc	cgt	gct	ggt														499
Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly														
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gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac														547
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp														
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Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro														
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Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile														
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Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu														
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Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met														
tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggg	cta	tcc	ttg	cca														787
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro														
aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggg	acg	gaa														835
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu														
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Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile														
acc	gaa	gcc	ggg	gac	ggg	att	acc	att	atc	aac	atc	ggg	gtg	ggc	cca														931
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro														
tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa														979
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu														
gcc	tgg	gtg	atg	atc	ggc	cac	tgt	gct	ggc	atg	gac	gcc	cgc	atg	cgc														
Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg														
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Ile	Gly	Asp	Leu	Ile	Leu	Gly	Asn	Ala	Tyr	Gln	Arg	Glu	Asp	His	Ile														

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa  
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu  
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc  
1168

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<212> PRT

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<400> 1052

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Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val  
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg  
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr  
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu  
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp  
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu  
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu  
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn  
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile  
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val  
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe  
195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val  
210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr  
225 230 235 240

Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro  
245 250 255

Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn  
260 265 270

Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala  
275 280 285

Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met  
290 295 300

Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln  
305 310 315 320

Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile  
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Ile Tyr Gly Ser  
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<212> DNA

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<220>

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<223> RXN01240

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Met Ser Asp Asn Thr  
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ctc tcc caa ttt ggc agt tac tac cac gaa ttc cga cgt gcc cat ccc 163  
Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe Arg Arg Ala His Pro  
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Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu Glu Leu Leu Thr Asp  
25 30 35

ggg ggt gtc acc ttc gat cgc gtc acc aca cgc atc aaa gaa tgg tca 259  
Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser  
40 45 50

agc ctg aaa gcc aag gct cgc aag cgt cgc aac gat ggc tcg ttg atc 307  
Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile  
55 60 65

tac cct gat ccg cgc aaa gac atc cac gac atg atc ggt gtt cgg atc	355
Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile	
70 75 80 85	
acc acg tac cac tcc acg gaa ata ccc gtg gcc cta aaa gtg ctc caa	403
Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln	
90 95 100	
gac tcc ttc atc gtc cac aaa tcc gta gac aaa gcc gct gaa act cgc	451
Asp Ser Phe Ile Val His Lys Ser Val Asp Lys Ala Ala Glu Thr Arg	
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Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His Leu Ile Leu Glu Val	
120 125 130	
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Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys Gly Leu Val Phe Glu	
135 140 145	
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Val Gln Val Arg Thr Val Leu Gln His Ala Trp Ala Glu Phe Glu His	
150 155 160 165	
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Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn Pro Glu Asp Phe Ser	
170 175 180	
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Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala Gly Leu Ile Glu Leu	
185 190 195	
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Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu Lys Glu Thr Ser Arg	
200 205 210	
gtt gct gat gaa tcc gtc gaa ctc acc gca gag aca ctt ccc ggc gtt	787
Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val	
215 220 225	
ctt gcc atg ctc att ggc aac cgc ttc ccc cgc cca cgc tcc aca aac	835
Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn	
230 235 240 245	
tac cgc ttc ctc gaa gac atc ctg gtg gcc aac tcc att acc tct gtg	883
Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val	
250 255 260	
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Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp Ile Glu Val Leu Leu	
265 270 275	
aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac	979
Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp	
280 285 290	
gat tta cta ctc aaa cga ttt ggc caa tca cac atc gat gcc acc gtc	1027
Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His Ile Asp Ala Thr Val	
295 300 305	



gcc acc gac tcc caa cca ctc aac gcc aaa cgc cac agg cag cta aaa  
1075

Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys  
310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac  
1123

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

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Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn  
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Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met  
65 70 75 80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala  
85 90 95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys  
100 105 110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His  
115 120 125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys  
130 135 140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp  
145 150 155 160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn  
165 170 175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala  
180 185 190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu  
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Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu

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Ser Ile Thr Ser	Val Val Gln Leu Arg	Glu Leu Leu Asn Pro Thr Asp
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Ile Glu Val Leu	Leu Lys Val Met Asn Tyr Arg	Phe His Pro Gly Gln
	275	280 285
Ile Arg Ile Ile	Asp Asp Leu Leu Leu Lys Arg	Phe Gly Gln Ser His
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Ile Asp Ala Thr	Val Ala Thr Asp Ser Gln Pro	Leu Asn Ala Lys Arg
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His Arg Gln Leu	Lys Arg Lys Leu Glu Leu Met	Thr Gln Ala His Leu
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 Val Tyr Ala Ala Ile  
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 Gly Val Val His Ser Leu Phe Asn Ala Leu Pro Gly Arg Phe Lys Asp  
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 Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln Ser Leu His Thr Thr  
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 Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val Gln Ala Arg Thr His  
 40 45 50  
 gac atg cac tac aac gcc gaa ttc ggc att gca gcg cac tgg cga tac 307  
 Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala Ala His Trp Arg Tyr  
 55 60 65  
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Met	Ala	Trp	Met	Arg	Gln	Leu	Leu	Asp	Trp	Gln	Lys	Glu	Ala	Ala	Asp		
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ccc	aac	gag	ttc	ctg	gac	agc	ctg	cgc	tac	gat	ctg	act	tcc	aag	cag	451	
Pro	Asn	Glu	Phe	Leu	Asp	Ser	Leu	Arg	Tyr	Asp	Leu	Thr	Ser	Lys	Gln		
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Ile	Phe	Val	Phe	Thr	Pro	Lys	Gly	Asp	Val	Val	Asn	Leu	Pro	Val	Asn		
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Ser	Thr	Pro	Val	Asp	Phe	Ala	Tyr	Ala	Val	His	Thr	Glu	Val	Gly	His		
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cgc	tgc	atc	ggc	gcc	aaa	atc	aac	ggc	aaa	ctg	gtc	gct	ttg	gaa	acg	595	
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Asn	Ala	Gly	Pro	Ser	Arg	Gly	Trp	Gln	Glu	Phe	Val	Val	Ser	Pro	Arg		
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Tyr	Leu	Glu	Ala	Gly	Arg	Asp	Ala	Leu	Ala	Ala	Val	Ile	Gln	Arg	Gly		
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Gly	Leu	Pro	Met	His	Arg	Leu	Phe	Thr	Ala	Ser	Ser	Met	Lys	Thr	Val		
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Gly	Ser	Gly	Ser	Val	Ser	Ala	Gln	His	Val	Val	Asn	Arg	Leu	Met	Ala		
			265				270						275				
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Ile	Phe	Gly	Asp	Glu	Glu	Asp	Ala	Glu	Asp	Ala	Leu	Val	Ala	Arg	Thr		
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cca	ttc	agc	gag	ctg	gtc	aac	tcc	cgt	gcc	acc	acg	gaa	agc	agc	acc	1027	
Pro	Phe	Ser	Glu	Leu	Val	Asn	Ser	Arg	Ala	Thr	Thr	Glu	Ser	Ser	Thr		
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 330 335 340  
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 Ser Leu His Thr Thr Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val  
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 Gln Ala Arg Thr His Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala  
 50 55 60  
 Ala His Trp Arg Tyr Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln  
 65 70 75 80  
 Ala Glu Val Asp Gln Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln  
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 Lys Glu Ala Ala Asp Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp  
 100 105 110  
 Leu Thr Ser Lys Gln Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val  
 115 120 125  
 Asn Leu Pro Val Asn Ser Thr Pro Val Asp Phe Ala Tyr Ala Val His  
 130 135 140  
 Thr Glu Val Gly His Arg Cys Ile Gly Ala Lys Ile Asn Gly Lys Leu  
 145 150 155 160

Val Ala Leu Glu Thr Lys Leu Lys Ser Gly Asp Arg Val Glu Val Phe  
 165 170 175  
 Thr Ser Lys Asp Gln Asn Ala Gly Pro Ser Arg Gly Trp Gln Glu Phe  
 180 185 190  
 Val Val Ser Pro Arg Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys  
 195 200 205  
 Glu Arg Arg Glu Glu Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala  
 210 215 220  
 Val Ile Gln Arg Gly Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser  
 225 230 235 240  
 Ser Met Lys Thr Val Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala  
 245 250 255  
 Leu Tyr Thr Ala Ile Gly Ser Gly Ser Val Ser Ala Gln His Val Val  
 260 265 270  
 Asn Arg Leu Met Ala Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala  
 275 280 285  
 Leu Val Ala Arg Thr Pro Phe Ser Glu Leu Val Asn Ser Arg Ala Thr  
 290 295 300  
 Thr Glu Ser Ser Thr Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met  
 305 310 315 320  
 Ala Lys Leu Ala Lys Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe  
 325 330 335  
 Gly Phe Val Thr Arg Gly Gly Gly Val Ser Val His Arg Thr Asp Cys  
 340 345 350  
 Thr Asn Val Glu Lys Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val  
 355 360 365  
 Ser Trp Ala Ser Glu Gly Gln Gly Ser Val  
 370 375

&lt;210&gt; 1057

&lt;211&gt; 1059

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1036)

&lt;223&gt; RXN01940

&lt;400&gt; 1057

ccagaatcaa tcaccgatac agtggcagcc aaagtcagg ctgaagaagc cgctcaagcc 60

gccagctaaa tccacaaact gaactaagga gttttaccct atg acc acc aag atc 115  
 Met Thr Thr Lys Ile  
 1 5

atc ctc gac tgc gat cca gga cac gac gac gct gta gcc atg ctg ctc	163
Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu	
10 15 20	
gca gcc ggc agc cca gaa att gaa ctg ctt gga atc acc acg gtc ggc	211
Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly	
25 30 35	
ggc aac cag acc ttg gac aag gtc acc cac aat acg cag gtc gta gcc	259
Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala	
40 45 50	
acc atc gct gat atc aat gcg ccc atc tac cgc ggt gtc acc cga cca	307
Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro	
55 60 65	
ttg gtg cgc ccc gtt gag gta gcc gaa gat atc cac ggc gat acc ggc	355
Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly	
70 75 80 85	
atg gaa atc cac aag tac gaa ctg cct gaa cca acc aag cag gta gaa	403
Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu	
90 95 100	
gac acc cac gcg gtg gat ttc atc atc gat acc atc atg aat aac gag	451
Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr Ile Met Asn Asn Glu	
105 110 115	
ccc ggc agc gta gcg ctg gtt ccc acc gga cca ctg acc aac atc gcg	499
Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro Leu Thr Asn Ile Ala	
120 125 130	
ctg gca gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt	547
Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val	
135 140 145	
gtc ctc atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct	595
Val Leu Met Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala	
150 155 160 165	
gaa ttc aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac	643
Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn	
170 175 180	
gaa aag tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg	691
Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala	
185 190 195	
ctc gca aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac	739
Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp	
200 205 210	
gtc gcc gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac	787
Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr	
215 220 225	
cag gac gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct	835
Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala	
230 235 240 245	
gtt gca tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca	883

Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro  
 250 255 260

ctc gat gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct 931  
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala  
 265 270 275

gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979  
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val  
 280 285 290

gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag  
 1027  
 Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys  
 295 300 305

cgc atc gga tagacctgtt cacaaggttg tta  
 1059  
 Arg Ile Gly  
 310

<210> 1058  
 <211> 312  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1058  
 Met Thr Thr Lys Ile Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala  
 1 5 10 15  
 Val Ala Met Leu Leu Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly  
 20 25 30  
 Ile Thr Thr Val Gly Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn  
 35 40 45  
 Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg  
 50 55 60  
 Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile  
 65 70 75 80  
 His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro  
 85 90 95  
 Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr  
 100 105 110  
 Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro  
 115 120 125  
 Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu  
 130 135 140  
 Arg Val Lys Glu Val Val Leu Met Gly Gly Tyr His Val Gly Asn  
 145 150 155 160  
 Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala  
 165 170 175

His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp  
 180 185 190  
 Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn  
 195 200 205  
 Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala  
 210 215 220  
 Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val  
 225 230 235 240  
 His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr  
 245 250 255  
 Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr  
 260 265 270  
 Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr  
 275 280 285  
 Thr Gln Val Ala Val Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val  
 290 295 300  
 Ile Asp Ala Val Lys Arg Ile Gly  
 305 310

<210> 1059  
 <211> 602  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(579)  
 <223> FRXA01940

<400> 1059  
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 Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala  
 1 5 10 15  
 gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt gtc ctc 96  
 Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu  
 20 25 30  
 atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc 144  
 Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe  
 35 40 45  
 aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag 192  
 Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys  
 50 55 60  
 tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca 240  
 Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala  
 65 70 75 80  
 aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac gtc gcc 288  
 Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala



85	90	95	
gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac cag gac			336
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp			
100	105	110	
gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct gtt gca			384
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala			
115	120	125	
tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca ctc gat			432
Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp			
130	135	140	
gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct gat ttc			480
Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe			
145	150	155	160
cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt gac ctg			528
Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu			
165	170	175	
gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag cgc atc			576
Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile			
180	185	190	
gga tagacctgtt cacaagggttg tta			602
Gly			

&lt;210&gt; 1060

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1060

Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala			
1	5	10	15

Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu			
20	25	30	

Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe			
35	40	45	

Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys			
50	55	60	

Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala			
65	70	75	80

Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala			
85	90	95	

Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp			
100	105	110	

Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala			
115	120	125	

Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp  
 130 135 140  
 Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe  
 145 150 155 160  
 Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu  
 165 170 175  
 Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile  
 180 185 190

Gly

<210> 1061  
 <211> 1026  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1003)  
 <223> RXA02559

<400> 1061  
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 aaccaaccc caaaaccaga aaacactaag ctcgtgagac atg att cct gtt ctc 115  
 Met Ile Pro Val Leu  
 1 5  
 atc gac tgc gac acc ggc atc gac gac gcc ctc gcc ctg atc tac ctg 163  
 Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu  
 10 15 20  
 gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211  
 Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr  
 25 30 35  
 acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259  
 Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala Ile Asn Thr Arg Trp  
 40 45 50  
 gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307  
 Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln  
 55 60 65  
 cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355  
 Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly  
 70 75 80 85  
 gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403  
 Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu  
 90 95 100  
 ggt gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451  
 Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr  
 105 110 115

aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499  
 Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro  
 120 125 130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547  
 Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn  
 135 140 145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595  
 Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala  
 150 155 160 165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643  
 Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu  
 170 175 180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691  
 Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu  
 185 190 195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739  
 Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met  
 200 205 210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787  
 Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu  
 215 220 225

gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835  
 Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile  
 230 235 240 245

cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883  
 Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro  
 250 255 260

ttg atg cgt ggc acc act gtt gca gat att cgc gga cat tgg ggc aag 931  
 Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys  
 265 270 275

cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979  
 Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His  
 280 285 290

gcg gaa ctt cta aga gca gtg gaa tgaaataatc cggtgctgat gca  
 1026  
 Ala Glu Leu Leu Arg Ala Val Glu  
 295 300

&lt;210&gt; 1062

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1062

Met Ile Pro Val Leu Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu  
 1 5 10 15

Ala Leu Ile Tyr Leu Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu  
 20 25 30

Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala  
 35 40 45  
 Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro  
 50 55 60  
 Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr  
 65 70 75 80  
 Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His  
 85 90 95  
 Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu  
 100 105 110  
 Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu  
 115 120 125  
 Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr  
 130 135 140  
 Leu Tyr Pro Gly Asn Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val  
 145 150 155 160  
 Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile  
 165 170 175  
 Thr Val Cys Ser Leu Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp  
 180 185 190  
 Ile Leu Ser Thr Leu Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu  
 195 200 205  
 His Leu Pro Glu Met Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln  
 210 215 220  
 Gly Glu Gly Tyr Leu Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile  
 225 230 235 240  
 Ala Leu Asp Lys Ile Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val  
 245 250 255  
 Glu Ala Asp Ser Pro Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg  
 260 265 270  
 Gly His Trp Gly Lys Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp  
 275 280 285  
 Ile Glu Ala Ala His Ala Glu Leu Leu Arg Ala Val Glu  
 290 295 300

&lt;210&gt; 1063

&lt;211&gt; 1050

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1027)

&lt;223&gt; RXA02497

&lt;400&gt; 1063

tcgatgccgc cgctggcgaa gactcgggga aacctaataaa taccgaagaa gaatttgacc 60

gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115  
 Val Arg Leu Gly Val  
 1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163  
 Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg  
 10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211  
 Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg  
 25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259  
 Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile  
 40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307  
 Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr  
 55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355  
 Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser  
 70 75 80 85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403  
 Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly  
 90 95 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451  
 Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe  
 105 110 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499  
 Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn  
 120 125 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547  
 Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu  
 135 140 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595  
 Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr  
 150 155 160 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643  
 His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu  
 170 175 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691  
 Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met  
 185 190 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739  
 Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe  
 200 205 210

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787  
 Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro  
 215 220 225

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835  
 His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala  
 230 235 240 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883  
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile  
 250 255 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931  
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu  
 265 270 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979  
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp  
 280 285 290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag  
 1027  
 Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu  
 295 300 305

taacatttac ccggaaagga gtt  
 1050

<210> 1064

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 1064

Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val  
 1 5 10 15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp  
 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile  
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala  
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr  
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val  
 85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu  
 100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala  
 115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser  
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly  
145 150 155 160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg  
165 170 175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu  
180 185 190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly  
195 200 205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro  
210 215 220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu  
225 230 235 240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala  
245 250 255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly  
260 265 270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val  
275 280 285

Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile  
290 295 300

Asp Lys Gly Leu Glu  
305

<210> 1065

<211> 2226

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2203)

<223> RXN01079

<400> 1065

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gactgcatcg ggaaccaccg tcgtgccacg cggagaccag atg gac ttc cac gct 115  
Met Asp Phe His Ala  
1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163  
Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe  
10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211  
Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn  
25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259

Gln	Asn	Thr	Val	Phe	Phe	His	Asn	Leu	Gln	Glu	Lys	Ile	Asp	Tyr	Leu	
	40						45					50				
ggt	gaa	aac	aag	tac	tat	gac	cca	atc	ggt	ctg	gac	aag	tac	gac	ttc	307
Val	Glu	Asn	Lys	Tyr	Tyr	Asp	Pro	Ile	Val	Leu	Asp	Lys	Tyr	Asp	Phe	
	55					60					65					
cag	ttc	atc	aag	gac	ctc	ttc	aag	cgc	gca	tac	gga	ttc	aag	ttc	cgc	355
Gln	Phe	Ile	Lys	Asp	Leu	Phe	Lys	Arg	Ala	Tyr	Gly	Phe	Lys	Phe	Arg	
	70				75					80					85	
ttc	cag	tcc	ttc	ctc	ggt	gca	tac	aag	tac	tac	act	tcc	tac	acc	ctg	403
Phe	Gln	Ser	Phe	Leu	Gly	Ala	Tyr	Lys	Tyr	Tyr	Thr	Ser	Tyr	Thr	Leu	
				90				95						100		
aag	acc	ttc	gac	ggt	cgc	cgc	tac	ctc	gag	cgt	ttc	gaa	gac	cgt	gtc	451
Lys	Thr	Phe	Asp	Gly	Arg	Arg	Tyr	Leu	Glu	Arg	Phe	Glu	Asp	Arg	Val	
			105					110					115			
tgc	atg	gtc	gcc	ctc	acc	ctc	gct	gac	ggc	gac	cgc	gca	ttg	gcc	gag	499
Cys	Met	Val	Ala	Leu	Thr	Leu	Ala	Asp	Gly	Asp	Arg	Ala	Leu	Ala	Glu	
		120					125					130				
aac	ctg	gtc	gat	gag	atc	atg	tct	ggc	cgt	ttc	caa	cca	gca	acc	cca	547
Asn	Leu	Val	Asp	Glu	Ile	Met	Ser	Gly	Arg	Phe	Gln	Pro	Ala	Thr	Pro	
	135					140					145					
acc	ttc	ctg	aac	tcc	ggc	aag	gca	cag	cgc	ggc	gag	cca	gta	tcc	tgc	595
Thr	Phe	Leu	Asn	Ser	Gly	Lys	Ala	Gln	Arg	Gly	Glu	Pro	Val	Ser	Cys	
	150				155					160					165	
ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643
Phe	Leu	Leu	Arg	Ile	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile	
				170					175					180		
aac	tct	gct	ctt	cag	ctg	tcc	aag	cgt	ggc	ggt	ggc	gta	gcg	ttg	ctg	691
Asn	Ser	Ala	Leu	Gln	Leu	Ser	Lys	Arg	Gly	Gly	Gly	Val	Ala	Leu	Leu	
			185					190					195			
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggt	gca	ccg	att	aag	aag	att	gaa	aac	739
Leu	Ser	Asn	Leu	Arg	Glu	Ala	Gly	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Asn	
		200					205					210				
cag	tct	tcc	ggt	gtt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787
Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe	
	215					220						225				
tcc	tac	gct	aac	cag	ctg	ggt	gct	cgt	cag	ggt	gca	ggt	gct	gtg	tac	835
Ser	Tyr	Ala	Asn	Gln	Leu	Gly	Ala	Arg	Gln	Gly	Ala	Gly	Ala	Val	Tyr	
	230				235					240					245	
ctc	aac	gct	cac	cac	cca	gat	atc	ctg	tcc	ttc	ctg	gat	acc	aag	cgt	883
Leu	Asn	Ala	His	His	Pro	Asp	Ile	Leu	Ser	Phe	Leu	Asp	Thr	Lys	Arg	
				250					255					260		
gag	aac	gcc	gat	gag	aag	atc	cgc	atc	aag	acc	ctg	tcc	ctg	ggt	gtt	931
Glu	Asn	Ala	Asp	Glu	Lys	Ile	Arg	Ile	Lys	Thr	Leu	Ser	Leu	Gly	Val	
			265					270						275		
gtg	att	ccg	gac	atc	acc	ttc	gag	ctg	gct	aag	cgc	aac	gat	gac	atg	979
Val	Ile	Pro	Asp	Ile	Thr	Phe	Glu	Leu	Ala	Lys	Arg	Asn	Asp	Asp	Met	



280	285	290
tac ctg ttc tcc cca tac gat gtg gag cgc att tac ggc aag cct ttc 1027		
Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile Tyr Gly Lys Pro Phe 295 300 305		
gca gac gtc tca atc acc gag cac tac gac gag atg gtg gat gat gac 1075		
Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu Met Val Asp Asp Asp 310 315 320 325		
cgc atc cgc aag acc aag atc aac gcg cgt cag ttc ttc cag acc ctg 1123		
Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln Phe Phe Gln Thr Leu 330 335 340		
gca gaa atc cag ttc gag tcc ggt tac cca tac atc atg tat gaa gac 1171		
Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr Ile Met Tyr Glu Asp 345 350 355		
acc gtg aat gca tcc aac cca atc gaa ggt cgc atc acc cac tca aac 1219		
Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg Ile Thr His Ser Asn 360 365 370		
ctg tgc tct gag atc ctt cag gtg tcc acc cca tct gaa ttc aac gat 1267		
Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro Ser Glu Phe Asn Asp 375 380 385		
gac ctg act tac gca gag gtc ggc gaa gac att tct tgt aac ttg ggt 1315		
Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile Ser Cys Asn Leu Gly 390 395 400 405		
tcc ctc aac gtt gca atg gct atg gat gca cca aac ttt gag aag acc 1363		
Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr 410 415 420		
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc 1411		
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser 425 430 435		
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc 1459		
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala 440 445 450		
atc ggc ctt ggc cag atg aac ctt cac ggc tac ttc ggt cgc gag cac 1507		
Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His 455 460 465		
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt 1555		
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe 470 475 480 485		

gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act  
1603

Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr  
490 495 500

gag cgt gga gag cgt ttc aag aac ttc gaa aac tcc aag tat gca acc  
1651

Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr  
505 510 515

ggg gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc  
1699

Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser  
520 525 530

gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc  
1747

Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr  
535 540 545

gtt gag gac tgg gct gcg ctg aag gcc gac gtg atg gag cac ggt ctg  
1795

Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu  
550 555 560 565

ttc aac cgt aac ctg caa gcg gtt cca cca acc ggt tcg atc tcc tac  
1843

Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr  
570 575 580

atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag  
1891

Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu  
585 590 595

atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac  
1939

Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His  
600 605 610

atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc  
1987

Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly  
615 620 625

tac gag aag atc att gac acc tac gct gtg gca acc aag tac gtt gac  
2035

Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp  
630 635 640 645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt  
2083

Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp Thr Ala Thr Thr Arg  
650 655 660

gac atc aac cgt gcg cag atc tac gca tgg cgc aag ggc atc aag acc  
2131

Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg Lys Gly Ile Lys Thr  
665 670 675

ttg tac tac att 'cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt  
2179

Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu Glu Gly Thr Glu Val  
680 685 690

gac ggc tgc gtc agc tgc atg ctg taaaagcact taaaaatatt ccc  
2226

Asp Gly Cys Val Ser Cys Met Leu  
695 700

<210> 1066

<211> 701

<212> PRT

<213> Corynebacterium glutamicum

<400> 1066

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn  
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Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe  
20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu  
35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu  
50 55 60

Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr  
65 70 75 80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr  
85 90 95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg  
100 105 110

Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp  
115 120 125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe  
130 135 140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly  
145 150 155 160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser  
165 170 175

Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly  
180 185 190

Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile  
195 200 205

Lys Lys Ile Glu Asn Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu  
210 215 220

Leu Glu Asp Ala Phe Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly  
225 230 235 240

Ala Gly Ala Val Tyr Leu Asn Ala His His Pro Asp Ile Leu Ser Phe  
 245 250 255  
 Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile Lys Thr  
 260 265 270  
 Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu Ala Lys  
 275 280 285  
 Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile  
 290 295 300  
 Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu  
 305 310 315 320  
 Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln  
 325 330 335  
 Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr  
 340 345 350  
 Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg  
 355 360 365  
 Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro  
 370 375 380  
 Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile  
 385 390 395 400  
 Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro  
 405 410 415  
 Asn Phe Glu Lys Thr Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val  
 420 425 430  
 Pro Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn  
 435 440 445  
 Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr  
 450 455 460  
 Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe  
 465 470 475 480  
 Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser  
 485 490 495  
 Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn  
 500 505 510  
 Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp  
 515 520 525  
 Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn  
 530 535 540  
 Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val  
 545 550 555 560

Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr  
565 570 575

Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile  
580 585 590

Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr  
595 600 605

Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp  
610 615 620

Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala  
625 630 635 640

Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp  
645 650 655

Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg  
660 665 670

Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu  
675 680 685

Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu  
690 695 700

<210> 1067

<211> 790

**<212> DNA**

<213> *Corynebacterium glutamicum*

**<220>**

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<222> (101) .. (790)

<223> FRXA01079

<400> 1067

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gactgcatcg'ggaaccaccg tcgtgccacg cggagaccag atg gac ttc cac gct 115  
Met Asp Phe His Ala  
1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163  
Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe  
10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211  
Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn  
25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259  
Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu  
40 45 50

gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc 307  
Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe  
55 60 65

cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355  
 Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg  
 70 75 80 85  
 ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403  
 Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu  
 90 95 100  
 aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451  
 Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val  
 105 110 115  
 tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499  
 Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu  
 120 125 130  
 aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547  
 Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro  
 135 140 145  
 acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595  
 Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys  
 150 155 160 165  
 ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc 643  
 Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile  
 170 175 180  
 aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg 691  
 Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu  
 185 190 195  
 ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa atc 739  
 Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Ile  
 200 205 210  
 cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc 787  
 Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe  
 215 220 225  
 tcc 790  
 Ser  
 230

&lt;210&gt; 1068

&lt;211&gt; 230

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1068

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn  
 1 5 10 15

Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe  
 20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu  
 35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu

50                      55                      60  
 Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr  
 65                      70                      75                      80  
 Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr  
                     85                      90                      95  
 Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg  
                     100                      105                      110  
 Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp  
                     115                      120                      125  
 Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe  
                     130                      135                      140  
 Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly  
 145                      150                      155                      160  
 Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser  
                     165                      170                      175  
 Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly  
                     180                      185                      190  
 Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile  
                     195                      200                      205  
 Lys Lys Ile Glu Ile Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu  
                     210                      215                      220  
 Leu Glu Asp Ala Phe Ser  
 225                      230

<210> 1069  
 <211> 1364  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1341)  
 <223> FRXA01084

<400> 1069  
 tcc ttt ctg gat acc aag cgc gag aac gcc gat gag aag atc cgc atc    48  
 Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile  
   1                      5                      10                      15  
 aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg    96  
 Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu  
                     20                      25                      30  
 gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag    144  
 Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu  
                     35                      40                      45  
 cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac    192  
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr

50	55	60	
gac gag atg gtg gat gat gac cgc atc cgc aag acc aag atc aac gcg Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala 65 70 75 80			240
cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr 85 90 95			288
cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu 100 105 110			336
ggg cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser 115 120 125			384
acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu 130 135 140			432
gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp 145 150 155 160			480
gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr 165 170 175			528
gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys 180 185 190			576
ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His 195 200 205			624
ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu 210 215 220			672
gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg 225 230 235 240			720
gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe 245 250 255			768
gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala 260 265 270			816
aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys 275 280 285			864
tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala 290 295 300			912



gac gtg atg gag cac ggt ctg ttc aac cgt aac ctg caa gcg gtt cca 960  
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro  
 305 310 315 320

cca acc ggt tcg atc tcc tac atc aac aac tcc acc tcg tcg atc cac  
 1008  
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His  
 325 330 335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc  
 1056  
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg  
 340 345 350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc  
 1104  
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe  
 355 360 365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct  
 1152  
 Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala  
 370 375 380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc  
 1200  
 Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe  
 385 390 395 400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca  
 1248  
 Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala  
 405 410 415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt  
 1296  
 Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val  
 420 425 430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg  
 1341  
 Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu  
 435 440 445

taaaagcact taaaaatatc ccc  
 1364

<210> 1070  
 <211> 447  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1070  
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 Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu  
 20 25 30

Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu  
 35 40 45  
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr  
 50 55 60  
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala  
 65 70 75 80  
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr  
 85 90 95  
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu  
 100 105 110  
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser  
 115 120 125  
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu  
 130 135 140  
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp  
 145 150 155 160  
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr  
 165 170 175  
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys  
 180 185 190  
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His  
 195 200 205  
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu  
 210 215 220  
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg  
 225 230 235 240  
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe  
 245 250 255  
 Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala  
 260 265 270  
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys  
 275 280 285  
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala  
 290 295 300  
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro  
 305 310 315 320  
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His  
 325 330 335  
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg  
 340 345 350  
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe

355	360	365	
Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala			
370	375	380	
Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe			
385	390	395	400
Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala			
	405	410	415
Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val			
	420	425	430
Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu			
	435	440	445
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<211> 1125			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
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<223> RXN01920			
<400> 1071			
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cgaaaagcaa aaaaatttgt agaagggaag agcgcaccta atg gct gct gat tct 115			
Met Ala Ala Asp Ser			
1 5			
gat ctc agt gtt cac gat gct tac tta aag gag cat gtt gca cct gta 163			
Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu His Val Ala Pro Val			
10 15 20			
aag gcg atc aac tgg aac tcc atc cca gat tcc aaa gat ctt gaa gtc 211			
Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser Lys Asp Leu Glu Val			
25 30 35			
tgg gat cgt ctg acc ggt aac ttc tgg ctc cca gaa aag gtc cca gta 259			
Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro Glu Lys Val Pro Val			
40 45 50			
tcc aac gac atc aag agc tgg gga acc ctc aac gag gtt gaa aaa gcc 307			
Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn Glu Val Glu Lys Ala			
55 60 65			
gca acc atg cgc gtg ttc acc gga ctt acc ctg ctg gac acc att cag 355			
Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu Leu Asp Thr Ile Gln			
70 75 80 85			
ggc act gtc ggc gca atc tcc ctg ctt cca gac gca gat tca ctg cac 403			
Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp Ala Asp Ser Leu His			
90 95 100			
gaa gaa gcg gtg cta acc aac att gcg ttc atg gaa tcc gtg cac gca 451			
Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met Glu Ser Val His Ala			

105										110										115										
aag	agt	tac	tcc	aac	atc	ttc	atg	act	ctg	gcc	tcc	acc	gcg	gaa	atc		499													
Lys	Ser	Tyr	Ser	Asn	Ile	Phe	Met	Thr	Leu	Ala	Ser	Thr	Ala	Glu	Ile															
		120					125					130																		
aac	gat	gcg	ttc	cgt	tgg	tct	gag	gaa	aat	gaa	aac	ctg	cag	cgc	aag		547													
Asn	Asp	Ala	Phe	Arg	Trp	Ser	Glu	Glu	Asn	Glu	Asn	Leu	Gln	Arg	Lys															
	135					140					145																			
gca	aag	atc	atc	ctg	tct	tac	tat	gag	ggc	gat	gat	cca	cta	aag	cgc		595													
Ala	Lys	Ile	Ile	Leu	Ser	Tyr	Tyr	Glu	Gly	Asp	Asp	Pro	Leu	Lys	Arg															
150					155				160						165															
aag	atc	gcc	tcc	gtg	atc	ctg	gag	tcc	ttc	ctg	ttc	tac	tcc	ggc	ttc		643													
Lys	Ile	Ala	Ser	Val	Ile	Leu	Glu	Ser	Phe	Leu	Phe	Tyr	Ser	Gly	Phe															
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tac	ctc	cca	atg	tat	tgg	tcc	agc	cac	tcc	aag	ctg	gcc	aac	acc	gcc		691													
Tyr	Leu	Pro	Met	Tyr	Trp	Ser	Ser	His	Ser	Lys	Leu	Ala	Asn	Thr	Ala															
			185					190					195																	
gac	gtg	atc	cgc	ctg	atc	atc	cgc	gat	gag	gca	gtg	cac	ggc	tac	tac		739													
Asp	Val	Ile	Arg	Leu	Ile	Ile	Arg	Asp	Glu	Ala	Val	His	Gly	Tyr	Tyr															
	200						205					210																		
att	ggc	tac	aag	tat	caa	aag	gct	gtc	gcg	aag	gag	act	cca	gag	cgt		787													
Ile	Gly	Tyr	Lys	Tyr	Gln	Lys	Ala	Val	Ala	Lys	Glu	Thr	Pro	Glu	Arg															
	215					220					225																			
cag	gaa	gag	ctg	aag	gag	tac	acc	ttc	gat	ctg	ctc	tac	gat	ctt	tac		835													
Gln	Glu	Glu	Leu	Lys	Glu	Tyr	Thr	Phe	Asp	Leu	Leu	Tyr	Asp	Leu	Tyr															
230					235					240					245															
gat	aac	gaa	act	cag	tac	tcc	gaa	gat	ctc	tac	gac	gat	ctt	gga	tgg		883													
Asp	Asn	Glu	Thr	Gln	Tyr	Ser	Glu	Asp	Leu	Tyr	Asp	Asp	Leu	Gly	Trp															
				250				255						260																
acc	gag	gat	gtt	aag	cga	ttc	ctt	cgc	tac	aac	gcc	aac	aag	gcc	ctc		931													
Thr	Glu	Asp	Val	Lys	Arg	Phe	Leu	Arg	Tyr	Asn	Ala	Asn	Lys	Ala	Leu															
			265					270					275																	
aac	aac	ctt	ggc	tac	gaa	gga	ctc	ttc	cca	gcg	gat	gaa	acc	aag	gtg		979													
Asn	Asn	Leu	Gly	Tyr	Glu	Gly	Leu	Phe	Pro	Ala	Asp	Glu	Thr	Lys	Val															
		280					285					290																		
tcc	cca	aac	atc	ttg	tct	gcg	ctg	tca	cca	aac	gct	gat	gag	aac	cac															
1027																														
Ser	Pro	Asn	Ile	Leu	Ser	Ala	Leu	Ser	Pro	Asn	Ala	Asp	Glu	Asn	His															
		295				300					305																			
gac	ttc	ttc	tcc	ggc	tcc	ggt	tcc	tct	tac	gtt	att	ggt	aag	gca	gaa															
1075																														
Asp	Phe	Phe	Ser	Gly	Ser	Gly	Ser	Ser	Tyr	Val	Ile	Gly	Lys	Ala	Glu															
310					315					320					325															
aac	acc	gag	gat	gat	gac	tgg	gac	ttc	taacttttaa	aaagctgaag																				
1122																														
Asn	Thr	Glu	Asp	Asp	Asp	Trp	Asp	Phe																						
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cgc  
1125

<210> 1072

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 1072

Met Ala Ala Asp Ser Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu  
1 5 10 15

His Val Ala Pro Val Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser  
20 25 30

Lys Asp Leu Glu Val Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro  
35 40 45

Glu Lys Val Pro Val Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn  
50 55 60

Glu Val Glu Lys Ala Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu  
65 70 75 80

Leu Asp Thr Ile Gln Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp  
85 90 95

Ala Asp Ser Leu His Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met  
100 105 110

Glu Ser Val His Ala Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala  
115 120 125

Ser Thr Ala Glu Ile Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu  
130 135 140

Asn Leu Gln Arg Lys Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp  
145 150 155 160

Asp Pro Leu Lys Arg Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu  
165 170 175

Phe Tyr Ser Gly Phe Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys  
180 185 190

Leu Ala Asn Thr Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala  
195 200 205

Val His Gly Tyr Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys  
210 215 220

Glu Thr Pro Glu Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu  
225 230 235 240

Leu Tyr Asp Leu Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr  
245 250 255

Asp Asp Leu Gly Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn  
260 265 270

Ala Asn Lys Ala Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala  
 275 280 285

Asp Glu Thr Lys Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn  
 290 295 300

Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val  
 305 310 315 320

Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
 325 330

&lt;210&gt; 1073

&lt;211&gt; 437

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(414)

&lt;223&gt; FRXA01920

&lt;400&gt; 1073

gcc gac gtg atc cgc ctg atc atc cgc gat gag gca gtg cac ggc tac 48  
 Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr  
 1 5 10 15

tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag 96  
 Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu  
 20 25 30

cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt 144  
 Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu  
 35 40 45

tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga 192  
 Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly  
 50 55 60

tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc 240  
 Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala  
 65 70 75 80

ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag 288  
 Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys  
 85 90 95

gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac 336  
 Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn  
 100 105 110

cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca 384  
 His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala  
 115 120 125

gaa aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag 434  
 Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
 130 135

cgc 437

&lt;210&gt; 1074

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1074

Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr  
 1 5 10 15

Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu  
 20 25 30

Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu  
 35 40 45

Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly  
 50 55 60

Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala  
 65 70 75 80

Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys  
 85 90 95

Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn  
 100 105 110

His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala  
 115 120 125

Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe  
 130 135

&lt;210&gt; 1075

&lt;211&gt; 567

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(544)

&lt;223&gt; RXA01080

&lt;400&gt; 1075

ttcagttctt cccttcaacg cccttgaagg gggaaactga taccagcaag cacactaggc 60

ttgcgcacaa acggtattta gaagggaagt gagttcgagg atg cta atc gtg tat 115  
 Met Leu Ile Val Tyr  
 1 5

ttt tcc tcg gcc acc gac aac acg cat cgt ttt gta caa aag ctc gat 163  
 Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe Val Gln Lys Leu Asp  
 10 15 20

tta ccc aac gtg cgc atc ccc ctc act agg gtg gaa gaa ccg ctg aaa 211  
 Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val Glu Glu Pro Leu Lys  
 25 30 35

atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259  
 Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val  
           40                          45                          50

tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307  
 Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg  
           55                          60                          65

ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca 355  
 Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala  
           70                          75                          80                          85

ggg gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc 403  
 Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile  
                           90                          95                          100

att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg 451  
 Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met  
                           105                          110                          115

ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac 499  
 Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn  
           120                          125                          130

gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga 544  
 Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg  
           135                          140                          145

taaaccttaa aacttaatca atc 567

&lt;210&gt; 1076

&lt;211&gt; 148

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1076

Met Leu Ile Val Tyr Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe  
   1                          5                          10                          15

Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val  
           20                          25                          30

Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr  
           35                          40                          45

Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro  
           50                          55                          60

Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile  
           65                          70                          75                          80

Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly  
                           85                          90                          95

Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr  
           100                          105                          110

Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly  
           115                          120                          125



Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro  
 130 135 140

Val Thr Ser Arg  
 145

<210> 1077

<211> 650

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(627)

<223> RXA00867

<400> 1077

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ttc ggc gac atg gac ttc aag gtt gcc ggc acc gca gac ttc atc acc 48
Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr
  1 5 10 15

gca ctt cag ctg gac acc aag ctg gac ggc att cct tcc aag gtg ctc 96
Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu
  20 25 30

tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac 144
Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn
  35 40 45

acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct 192
Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala
  50 55 60

cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg 240
Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu
  65 70 75 80

atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc 288
Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly
  85 90 95

gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct 336
Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala
  100 105 110

gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg 384
Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala
  115 120 125

aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc 432
Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val
  130 135 140

aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac 480
Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp
  145 150 155 160

ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag 528
Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys
  165 170 175

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gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct 576  
 Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala  
                   180                  185                  190

gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag 624  
 Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu  
                   195                  200                  205

gac taattagttc tggctagatc ggg 650  
 Asp

<210> 1078

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 1078

Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr  
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Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu  
                   20                  25                  30

Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn  
                   35                  40                  45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala  
                   50                  55                  60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu  
                   65                  70                  75                  80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly  
                   85                  90                  95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala  
                   100                  105                  110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala  
                   115                  120                  125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val  
                   130                  135                  140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp  
                   145                  150                  155                  160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys  
                   165                  170                  175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala  
                   180                  185                  190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu  
                   195                  200                  205

Asp

&lt;210&gt; 1079

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(630)

&lt;223&gt; RXA01416

&lt;400&gt; 1079

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gct ggc gct tcc gaa aac gtt gtc aac cgc gtc aag gac ggt gca cca      48
Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro
  1              5              10              15

gca cca acc gaa aag atc gtc tcc gac ggc ctt gaa gca gct aag cca      96
Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro
              20              25              30

ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt     144
Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
              35              40              45

gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag     192
Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
              50              55              60

gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg     240
Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu
              65              70              75              80

ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac     288
Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
              85              90              95

atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac     336
Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
              100              105              110

agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct     384
Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
              115              120              125

gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc     432
Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
              130              135              140

atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt     480
Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val
              145              150              155              160

gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag     528
Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
              165              170              175

acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag     576
Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
              180              185              190

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caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac 624  
 Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His  
           195                          200                          205

tac aac 630  
 Tyr Asn  
           210

<210> 1080

<211> 210

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1080

Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro  
       1                          5                          10                          15

Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro  
                           20                          25                          30

Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val  
                           35                          40                          45

Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu  
                           50                          55                          60

Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu  
                           65                          70                          75                          80

Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr  
                           85                          90                          95

Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr  
                           100                          105                          110

Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala  
                           115                          120                          125

Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg  
                           130                          135                          140

Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val  
                           145                          150                          155                          160

Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu  
                           165                          170                          175

Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln  
                           180                          185                          190

Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His  
                           195                          200                          205

Tyr Asn  
           210

<210> 1081

<211> 757

<212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(757)

&lt;223&gt; RXA01486

&lt;400&gt; 1081

agagaactgg taagggtttt accgttctag accgcagaaa tcttcgcggc gacaccgatg 60

atcgccgagc	agaactaaac	atgaggagac	ctactcgc	atg	agc	gat	gta	aag	115
				Met	Ser	Asp	Val	Lys	
				1				5	

gac	ttc	gaa	gac	acc	gaa	ttt	ggc	ctg	atc	gag	gcc	gtc	gca	acc	atc	163
Asp	Phe	Glu	Asp	Thr	Glu	Phe	Gly	Leu	Ile	Glu	Ala	Val	Ala	Thr	Ile	
				10					15					20		

gac	aac	ggg	gac	ttc	gga	acc	cgc	acc	atc	cgt	ttt	gaa	acc	ggc	caa	211
Asp	Asn	Gly	Asp	Phe	Gly	Thr	Arg	Thr	Ile	Arg	Phe	Glu	Thr	Gly	Gln	
				25				30						35		

ctt	gcc	cgc	cag	gca	gat	ggg	gca	gtg	acc	acc	tac	ctc	gac	gat	gac	259
Leu	Ala	Arg	Gln	Ala	Asp	Gly	Ala	Val	Thr	Thr	Tyr	Leu	Asp	Asp	Asp	
			40				45						50			

acg	atg	ctg	ctg	gca	acc	acc	acc	gca	tcc	aac	cag	cca	cgc	gag	ggc	307
Thr	Met	Leu	Leu	Ala	Thr	Thr	Ala	Ser	Asn	Gln	Pro	Arg	Glu	Gly		
	55					60				65						

ttt	gac	ttc	ttc	cca	ctg	acc	gtg	gac	gtt	gaa	gag	cgt	atg	tac	gca	355
Phe	Asp	Phe	Phe	Pro	Leu	Thr	Val	Asp	Val	Glu	Glu	Arg	Met	Tyr	Ala	
	70				75					80					85	

gct	ggg	cgc	atc	cct	ggc	tct	ttc	ttc	cgt	cgg	gag	ggg	cgc	cca	tcc	403
Ala	Gly	Arg	Ile	Pro	Gly	Ser	Phe	Phe	Arg	Arg	Glu	Gly	Arg	Pro	Ser	
				90					95					100		

acc	gaa	gct	atc	ctg	gct	tgc	cgt	ctc	atc	gac	cgc	cca	ctg	cgc	cca	451
Thr	Glu	Ala	Ile	Leu	Ala	Cys	Arg	Leu	Ile	Asp	Arg	Pro	Leu	Arg	Pro	
			105					110					115			

acc	ttt	gtt	aag	ggc	ctg	cgc	aat	gag	gtt	cag	atc	gtt	gtc	acc	gtc	499
Thr	Phe	Val	Lys	Gly	Leu	Arg	Asn	Glu	Val	Gln	Ile	Val	Val	Thr	Val	
		120					125					130				

atg	tcc	atg	aac	cct	gag	gat	tac	tac	gat	gtc	gta	gca	atc	aac	gga	547
Met	Ser	Met	Asn	Pro	Glu	Asp	Tyr	Tyr	Asp	Val	Val	Ala	Ile	Asn	Gly	
	135					140					145					

gct	tcc	gca	gca	acc	cgc	atc	tcc	gga	ctt	cct	gtc	tcc	ggc	gct	gtc	595
Ala	Ser	Ala	Ala	Thr	Arg	Ile	Ser	Gly	Leu	Pro	Val	Ser	Gly	Ala	Val	
	150				155					160				165		

ggg	ggc	gtt	cgc	atg	gca	ctg	gtt	ggg	gat	gaa	aag	cac	cca	gaa	ggc	643
Gly	Gly	Val	Arg	Met	Ala	Leu	Val	Gly	Asp	Glu	Lys	His	Pro	Glu	Gly	
				170				175						180		

caa	tgg	gtt	gca	ttc	cca	acc	cac	gct	caa	cat	gag	cag	tcc	gta	ttt	691
Gln	Trp	Val	Ala	Phe	Pro	Thr	His	Ala	Gln	His	Glu	Gln	Ser	Val	Phe	
			185					190					195			

gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739  
 Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg Lys Arg Gly Asn Lys  
           200                          205                          210

acc ttc tcc gac gtc gca 757  
 Thr Phe Ser Asp Val Ala  
           215

<210> 1082

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1082

Met Ser Asp Val Lys Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu  
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Ala Val Ala Thr Ile Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg  
                           20                          25                          30

Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr  
                           35                          40                          45

Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn  
           50                          55                          60

Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu  
       65                          70                          75                          80

Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg  
                           85                          90                          95

Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp  
                           100                          105                          110

Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln  
                           115                          120                          125

Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val  
       130                          135                          140

Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro  
       145                          150                          155                          160

Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu  
                           165                          170                          175

Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His  
                           180                          185                          190

Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg  
                           195                          200                          205

Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala  
       210                          215

<210> 1083

<211> 651

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(628)

&lt;223&gt; RXA01678

&lt;400&gt; 1083

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cggctatatc	tctgcaactg	cagctcaccc	cggtgcagca	atg	ctg	aaa	tgt	gca	115
				Met	Leu	Lys	Cys	Ala	
				1				5	

gtc	gat	gaa	gcc	gct	ggc	gga	cgc	gcc	caa	gct	ttc	gta	tcc	tca	ggc	163
Val	Asp	Glu	Ala	Ala	Gly	Gly	Arg	Ala	Gln	Ala	Phe	Val	Ser	Ser	Gly	
				10				15						20		

gat	aac	att	ggt	ggc	agc	ccg	ttc	caa	tcc	tcc	att	ctt	ggt	gat	gaa	211
Asp	Asn	Ile	Gly	Gly	Ser	Pro	Phe	Gln	Ser	Ser	Ile	Leu	Gly	Asp	Glu	
			25					30					35			

ccc	acc	ttg	gaa	gca	ctc	aac	caa	atg	ggt	ctt	gat	tac	tca	gca	gtg	259
Pro	Thr	Leu	Glu	Ala	Leu	Asn	Gln	Met	Gly	Leu	Asp	Tyr	Ser	Ala	Val	
		40					45					50				

ggc	aac	cac	gaa	ttt	gat	aaa	ggc	tac	gca	gac	tta	agc	agt	cga	gtc	307
Gly	Asn	His	Glu	Phe	Asp	Lys	Gly	Tyr	Ala	Asp	Leu	Ser	Ser	Arg	Val	
	55					60					65					

gct	gac	ctt	gct	gat	ttt	gat	tat	ctc	ggc	gca	aac	gtt	gag	ggc	gaa	355
Ala	Asp	Leu	Ala	Asp	Phe	Asp	Tyr	Leu	Gly	Ala	Asn	Val	Glu	Gly	Glu	
	70				75					80					85	

aac	cca	gat	ctt	gca	cca	tat	gga	att	tct	cac	ctt	gat	ggt	gtg	aag	403
Asn	Pro	Asp	Leu	Ala	Pro	Tyr	Gly	Ile	Ser	His	Leu	Asp	Gly	Val	Lys	
			90					95						100		

gtt	gct	ttc	gta	ggc	acc	gta	tcc	caa	gaa	act	ccg	atg	ttg	gtc	aat	451
Val	Ala	Phe	Val	Gly	Thr	Val	Ser	Gln	Glu	Thr	Pro	Met	Leu	Val	Asn	
			105					110					115			

tct	gaa	ggc	att	gag	gga	atc	acg	ttt	act	gac	cca	ctt	gaa	gca	acc	499
Ser	Glu	Gly	Ile	Glu	Gly	Ile	Thr	Phe	Thr	Asp	Pro	Leu	Glu	Ala	Thr	
		120					125					130				

aac	cgt	gta	gct	gat	gaa	ctc	gtg	gga	agt	ggc	gca	gca	gat	gtt	gtc	547
Asn	Arg	Val	Ala	Asp	Glu	Leu	Val	Gly	Ser	Gly	Ala	Ala	Asp	Val	Val	
	135					140					145					

gtt	gcg	ctt	tac	cac	gaa	ggc	att	acc	ggc	acc	gaa	gca	tgg	tca	gaa	595
Val	Ala	Leu	Tyr	His	Glu	Gly	Ile	Thr	Gly	Thr	Glu	Ala	Trp	Ser	Glu	
	150				155				160						165	

aat	atc	gac	gtt	gtt	ttc	gca	ggt	cac	acc	cac	taagttcgtg	atctaggaac	648
Asn	Ile	Asp	Val	Val	Phe	Ala	Gly	His	Thr	His			
			170					175					

cga

651

<210> 1084  
 <211> 176  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1084

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Met Leu Lys Cys Ala Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala
 1             5             10             15

Phe Val Ser Ser Gly Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser
      20             25             30

Ile Leu Gly Asp Glu Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu
      35             40             45

Asp Tyr Ser Ala Val Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp
      50             55             60

Leu Ser Ser Arg Val Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala
      65             70             75             80

Asn Val Glu Gly Glu Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His
      85             90             95

Leu Asp Gly Val Lys Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr
      100            105            110

Pro Met Leu Val Asn Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp
      115            120            125

Pro Leu Glu Ala Thr Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly
      130            135            140

Ala Ala Asp Val Val Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr
      145            150            155            160

Glu Ala Trp Ser Glu Asn Ile Asp Val Val Phe Ala Gly His Thr His
      165            170            175
  
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<210> 1085  
 <211> 1359  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1336)

<223> RXA01679

<400> 1085

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ctaagttcgt gatctaggaa ccgacaacgg tccactaatc atg cag tct gga aac 115
              Met Gln Ser Gly Asn
              1             5
  
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tac ggg cac gca ctt gcc gat gta gat ttc agc ttc aac cac gac acc	163
Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr	
10 15 20	
ggt gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc	211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Asp Ile	
25 30 35	
aac gcg tgt gaa aac cca gat gac acc att gca gat att gtt gct cag	259
Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala Asp Ile Val Ala Gln	
40 45 50	
gcg gaa ctt gat gct ggt gaa gcc ggc aaa gaa gta gta gcg acc atc	307
Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu Val Val Ala Thr Ile	
55 60 65	
gat ggc gat ttt ctc cgc gcc agc gac gaa gga gca gaa tct ggc tcc	355
Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly Ala Glu Ser Gly Ser	
70 75 80 85	
aac tac ggc gct gaa tcc cag ctc gtc aac atg att gcc agt gct gtg	403
Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met Ile Ala Ser Ala Val	
90 95 100	
cgt tgg tcc atg tcc acc aat acc gcc acc acc gca gac att ggg ctt	451
Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr Ala Asp Ile Gly Leu	
105 110 115	
atg aac gcc gga gga ctc cac act gac cta ttc agc ggc gat gtt acc	499
Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe Ser Gly Asp Val Thr	
120 125 130	
tac gcc gaa gct ttt gaa atc cag cct ttc tcc ggt gaa gat tca ttt	547
Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser Gly Glu Asp Ser Phe	
135 140 145	
gtc acc ctc aag gga tca gtc ttc aaa gat gcc ctt gac cag cag tgg	595
Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala Leu Asp Gln Gln Trp	
150 155 160 165	
gaa gaa ggt tct gca cga cca gtg gca gca ctt ggc gta tcc gac aac	643
Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu Gly Val Ser Asp Asn	
170 175 180	
gtt tcc tac acc tac gac atc aac cgt cca atc ggt gac cgc gtc act	691
Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile Gly Asp Arg Val Thr	
185 190 195	
tcc gtg acc att gat gat acc cca ctt gat ccg gaa cgc gac tac gtt	739
Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro Glu Arg Asp Tyr Val	
200 205 210	
gtt gca gct tcc ctg tac ctc cag tcc ggc aac gaa ggt atg acc gca	787
Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn Glu Gly Met Thr Ala	
215 220 225	
ctg acc cgc gga acc gca cct gca caa acc ggc atc gtg gat gta cag	835
Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly Ile Val Asp Val Gln	
230 235 240 245	
tcc acc atc gga tac ttg tcc aac aac aat gtc acc cca cgt act ggt	883

Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val Thr Pro Arg Thr Gly  
 250 255 260  
 caa gcc cag att tcc atc acc cca tcc ggt gag ttc aat gcg ggt gaa 931  
 Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu Phe Asn Ala Gly Glu  
 265 270 275  
 acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979  
 Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr  
 280 285 290  
 gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca  
 1027  
 Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro  
 295 300 305  
 att gat cct cag ctc gga gaa gct ggc ttt ggc gaa gct gga acc gcg  
 1075  
 Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala  
 310 315 320 325  
 aca gtg agc ttg gac att cct gca acc ctt tca ggt act caa aac ctc  
 1123  
 Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser Gly Thr Gln Asn Leu  
 330 335 340  
 gtt gtc acc acc gat acc ggc acc cgt att tcc atg cca gtt gag att  
 1171  
 Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser Met Pro Val Glu Ile  
 345 350 355  
 gtt ggc gca gaa caa cca gca ccg caa cca gca ggt tcc tct gtt tta  
 1219  
 Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala Gly Ser Ser Val Leu  
 360 365 370  
 gga act gga gtg ctc agt gga ctc ctc ggc att gtt gta gga att cta  
 1267  
 Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile Val Val Gly Ile Leu  
 375 380 385  
 gga atg gtc ggt ctg gtg aac tgg att gac cca agc ttc att caa cag  
 1315  
 Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln  
 390 395 400 405  
 atc cag cag caa atc ttt gct taaatttagt aaaaagcatg cat  
 1359  
 Ile Gln Gln Gln Ile Phe Ala  
 410

&lt;210&gt; 1086

&lt;211&gt; 412

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1086

Met Gln Ser Gly Asn Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser  
 1 5 10 15

Phe Asn His Asp Thr Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu  
 20 25 30  
 Gly Val Asp Asp Ile Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala  
 35 40 45  
 Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu  
 50 55 60  
 Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly  
 65 70 75 80  
 Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met  
 85 90 95  
 Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr  
 100 105 110  
 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe  
 115 120 125  
 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser  
 130 135 140  
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala  
 145 150 155 160  
 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu  
 165 170 175  
 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile  
 180 185 190  
 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro  
 195 200 205  
 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn  
 210 215 220  
 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly  
 225 230 235 240  
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val  
 245 250 255  
 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu  
 260 265 270  
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr  
 275 280 285  
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu  
 290 295 300  
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly  
 305 310 315 320  
 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser  
 325 330 335  
 Gly Thr Gln Asn Leu Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser

340	345	350
Met Pro Val Glu Ile Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala		
355	360	365
Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile		
370	375	380
Val Val Gly Ile Leu Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro		
385	390	395
400		
Ser Phe Ile Gln Gln Ile Gln Gln Gln Ile Phe Ala		
405	410	

&lt;210&gt; 1087

&lt;211&gt; 1071

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1048)

&lt;223&gt; RXN01488

&lt;400&gt; 1087

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gcccgcacctt aaaaataaaa acctgaaagg ttaaaaacgc atg agc aaa aaa gcc 115
                                     Met Ser Lys Lys Ala
                                     1           5
atc ctt gat atc gac acc ggc atc gat gat gcc ctc gca ctt gcc tac 163
Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ala Tyr
                10           15           20
gca ctg ggc tca cct gaa cta gag ctc att ggt gtc acc acc acc tac 211
Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly Val Thr Thr Thr Tyr
                25           30           35
ggt aac gtg cta ctc gaa acc ggt gca gtc aat gac ctg gca ctg ctt 259
Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu
                40           45           50
gat ctg ttc ggt gca cca gaa gta cct gtg tac ttg ggt gag cca cac 307
Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His
                55           60           65
gca cag acc aag gat ggc ttt gaa gtt ctt gag atc tcc gcg ttc att 355
Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile
                70           75           80           85
cac gga caa aac ggc atc ggc gaa gtc gag ctg cca gca agc gag tca 403
His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser
                90           95           100
aag gca ctc ccc ggc gca gtg gat ttc ctc att gat tcc gtc aac acc 451
Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr
                105           110           115
cac ggc gat gac ctg gtg atc atc gca act ggt ccc atg acc aac ctg 499

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His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu  
 120 125 130

tct gcg gca atc gca aag gat cca agc ttt gct tcc aag gct cac gtg 547  
 Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val  
 135 140 145

gtc atc atg ggt ggc gcc ttg act gtc cca ggc aac gtc agc aca tgg 595  
 Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp  
 150 155 160 165

gca gaa gca aac atc aac cag gac cca gat gca gca aac gat ctg ttc 643  
 Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe  
 170 175 180

cgt tcc ggt gca gat gtc acc atg atc ggt ctt gat gtc acc ctg cag 691  
 Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln  
 185 190 195

acc.ctt ctt acc aag aag cac act gcg cag tgg cgc gaa ctg ggc act 739  
 Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr  
 200 205 210

cca gct gct atc gca ctg gcc gac atg act gat tac tac atc aag gca 787  
 Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala  
 215 220 225

tat gag acc acc gca cca cac ctg ggc ggt tgc ggc ctg cac gac cca 835  
 Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro  
 230 235 240 245

ctg gca gta ggc gtt gca gtg gac cca agc ctg gtc act.ttg ctc ccc 883  
 Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro  
 250 255 260

atc aac ctc aag gta gac att gag ggc gag acc cgt gga cgc acc att 931  
 Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile  
 265 270 275

ggc gat gaa gtc cgc ctc aac gat cca gtg cgc acc tcc cgc gca gct 979  
 Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala  
 280 285 290

gtc gcc gta gac gtg gat cgt ttc ctt tct gaa ttc atg acc cgc atc  
 1027  
 Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile  
 295 300 305

ggc cga gtc gca gca cag cag taaaagcagc tctggtgaag gtt  
 1071  
 Gly Arg Val Ala Ala Gln Gln  
 310 315

<210> 1088  
 <211> 316  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1088  
 Met Ser Lys Lys Ala Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala

1	5	10	15
Leu Ala Leu Ala Tyr Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly	20	25	30
Val Thr Thr Thr Tyr Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn	35	40	45
Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr	50	55	60
Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu	65	70	75
Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu	85	90	95
Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile	100	105	110
Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly	115	120	125
Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala	130	135	140
Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly	145	150	155
Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala	165	170	175
Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu	180	185	190
Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp	195	200	205
Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp	210	215	220
Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys	225	230	235
Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu	245	250	255
Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr	260	265	270
Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg	275	280	285
Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu	290	295	300
Phe Met Thr Arg Ile Gly Arg Val Ala Ala Gln Gln	305	310	315

&lt;210&gt; 1089

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(343)

&lt;223&gt; RXC00540

&lt;400&gt; 1089

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aaacattgtc ctccccattt cttgagtaag ggaaaatacc gtg gcc cgt gta gtt 115  
 Val Ala Arg Val Val  
 1 5

gtc aat gtc atg cct aag gct gag att ctg gat ccc cag ggg cag gcg 163  
 Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp Pro Gln Gly Gln Ala  
 10 15 20

gta cac cgc gcc ctc gga cgt atc gga gtt tct ggc gtt tcc gat gtc 211  
 Val His Arg Ala Leu Gly Arg Ile Gly Val Ser Gly Val Ser Asp Val  
 25 30 35

cgt cag gga aag cgc ttc gag ctt gag gta gat gat tcc gtc acc gaa 259  
 Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp Asp Ser Val Thr Glu  
 40 45 50

gct gac cta aag aaa att gct gaa acc ctc ctc gca aac acc gtc atc 307  
 Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu Ala Asn Thr Val Ile  
 55 60 65

gaa gac ttc gat gtg gtg gga gtt gag gtc gcg aag tgagcgccaa 353  
 Glu Asp Phe Asp Val Val Gly Val Glu Val Ala Lys  
 70 75 80

aatcggtgtc att 366

&lt;210&gt; 1090

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1090

Val Ala Arg Val Val Val Asn Val Met Pro Lys Ala Glu Ile Leu Asp  
 1 5 10 15

Pro Gln Gly Gln Ala Val His Arg Ala Leu Gly Arg Ile Gly Val Ser  
 20 25 30

Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp  
 35 40 45

Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu  
 50 55 60

Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala  
 65 70 75 80

Lys

<210> 1091  
<211> 498  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<220>  
<221> CDS  
<222> (101)..(475)  
<223> RXC00560
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<400> 1091																	
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catatggaca				ctttaacggt	tcgtactagg	ctgatgcttc	atg	agg	att	gat	ccg						115
							Met	Arg	Ile	Asp	Pro						
							1				5						
ctg	gaa	acc	cgg	caa	gcc	gta	ttg	gcc	gtc	aaa	gac	tgg	att	gaa	ggg	163	
Leu	Glu	Thr	Arg	Gln	Ala	Val	Leu	Ala	Val	Lys	Asp	Trp	Ile	Glu	Gly		
				10					15					20			
gag	gga	gac	gtc	aaa	aag	cct	ggt	cgt	gcg	gca	ctt	gcc	gcc	gca	act	211	
Glu	Gly	Asp	Val	Lys	Lys	Pro	Gly	Arg	Ala	Ala	Leu	Ala	Ala	Ala	Thr		
				25					30					35			
cgc	ctg	agc	gtc	cga	ctg	ctc	gcg	caa	cac	gcg	ccg	gga	aac	agc	gtg	259	
Arg	Leu	Ser	Val	Arg	Leu	Leu	Ala	Gln	His	Ala	Pro	Gly	Asn	Ser	Val		
				40					45					50			
gag	gtg	cgg	gta	ccc	cca	ttt	gtt	gcg	gtg	caa	tgc	ata	gag	ggg	cca	307	
Glu	Val	Arg	Val	Pro	Pro	Phe	Val	Ala	Val	Gln	Cys	Ile	Glu	Gly	Pro		
				55					60					65			
aaa	cat	aca	cgc	ggc	aca	cca	ccc	aac	gtg	gtg	gag	acc	gac	gcc	aag	355	
Lys	His	Thr	Arg	Gly	Thr	Pro	Pro	Asn	Val	Val	Glu	Thr	Asp	Ala	Lys		
				70					75					80			
acc	tgg	tta	cgc	tta	gca	cct	ggg	caa	acc	aca	ttt	gat	gca	gaa	ttt	403	
Thr	Trp	Leu	Arg	Leu	Ala	Pro	Gly	Gln	Thr	Thr	Phe	Asp	Ala	Glu	Phe		
				90					95					100			
gaa	agc	gga	aaa	att	agc	gca	tca	ggt	acc	cga	gcc	aaa	gag	att	gcg	451	
Glu	Ser	Gly	Lys	Ile	Ser	Ala	Ser	Gly	Thr	Arg	Ala	Lys	Glu	Ile	Ala		
				105					110					115			
gac	tgg	tta	cca	gtg	gtc	aaa	ctt	tagatttcct aatgctcatt agt							498		
Asp	Trp	Leu	Pro	Val	Val	Lys	Leu										
				120					125								

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<210> 1092
<211> 125
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1092  
Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys  
1 5 10 15



Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala  
                   20                                  25                                  30  
 Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala  
                   35                                  40                                  45  
 Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln  
                   50                                  55                                  60  
 Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val  
                   65                                  70                                  75                                  80  
 Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr  
                   85                                  90                                  95  
 Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg  
                   100                                  105                                  110  
 Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu  
                   115                                  120                                  125

&lt;210&gt; 1093

&lt;211&gt; 1305

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1282)

&lt;223&gt; RXC01088

&lt;400&gt; 1093

tgccttgagt ctaattctcc cgcccgtagc atgggtttaa gctggactga taaacctttt 60  
 gtgaaccgaa ttttttaact gatttgaaga agcgagaata atg gga ctg tgg atc 115  
   Met Gly Leu Trp Ile  
   1                                  5  
 gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163  
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile  
                                   10                                  15                                  20  
 gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211  
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val  
                                   25                                  30                                  35  
 atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259  
 Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly  
                                   40                                  45                                  50  
 caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat 307  
 Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His  
                                   55                                  60                                  65  
 cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc 355  
 His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile  
                                   70                                  75                                  80                                  85  
 cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct 403

Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala  
90 95 100

atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc 451  
Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe  
105 110 115

cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc 499  
His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys  
120 125 130

gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att 547  
Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile  
135 140 145

gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg 595  
Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His Gly Asp Ile Pro Val  
150 155 160 165

cca gtt cca gcc gtg gca gag ctg gtg aaa ggc tgg ccc acc caa acc 643  
Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly Trp Pro Thr Gln Thr  
170 175 180

gga gct ctt atg gag agc acc gaa cct gtt ggt gaa tta gcc acc cca 691  
Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly Glu Leu Ala Thr Pro  
185 190 195

act ggt gtt gcg ttg atc cgt cac ttt gcc acc caa gat ggc cct ttc 739  
Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr Gln Asp Gly Pro Phe  
200 205 210

cca ggt ggc atc atc aat gaa gtt ggc att ggt gca gga aca aaa gat 787  
Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly Ala Gly Thr Lys Asp  
215 220 225

aca gaa ggc cgt cca aat ata gtg cgc gca att ttg ttc aac acc tct 835  
Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile Leu Phe Asn Thr Ser  
230 235 240 245

agg agt aac cca gat acc cgc aca ctg gtg caa tta gaa gcc aat gtt 883  
Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln Leu Glu Ala Asn Val  
250 255 260

gat gat caa gac cca cgg ctg tgg cca gga gta ata gag atc ctc ttt 931  
Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val Ile Glu Ile Leu Phe  
265 270 275

gcc gct ggc gca gta gat gca tgg ctg act cca att ttg atg aag aag 979  
Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro Ile Leu Met Lys Lys  
280 285 290

ggc cgt cct gca cat agg gtg tca gca ttg gtg gat agc tcc gag gtg  
1027  
Gly Arg Pro Ala His Arg Val Ser Ala Leu Val Asp Ser Ser Glu Val  
295 300 305

gaa gca gtg aaa acc gca tta ttt gca gcc acc acg act ttt ggg atc  
1075  
Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr Thr Thr Phe Gly Ile  
310 315 320 325

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa  
1123

Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln  
330 335 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat  
1171

Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp  
345 350 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca  
1219

Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala  
360 365 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg  
1267

Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro  
375 380 385

caa ggc acc acc gag taacaaccaa aaggtcgact gct  
1305

Gln Gly Thr Thr Glu  
390

<210> 1094

<211> 394

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1094

Met Gly Leu Trp Ile Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu  
1 5 10 15

Leu Gly Ala Leu Ile Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln  
20 25 30

Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu  
35 40 45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln  
50 55 60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu  
65 70 75 80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val  
85 90 95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro  
100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp  
115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile  
130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His  
145 150 155 160

Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly  
 165 170 175  
 Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly  
 180 185 190  
 Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr  
 195 200 205  
 Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly  
 210 215 220  
 Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile  
 225 230 235 240  
 Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln  
 245 250 255  
 Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val  
 260 265 270  
 Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro  
 275 280 285  
 Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val  
 290 295 300  
 Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr  
 305 310 315 320  
 Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp  
 325 330 335  
 Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys  
 340 345 350  
 Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu  
 355 360 365  
 Asp Ile Arg Ser Ala Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val  
 370 375 380  
 Val Ala Arg Ile Pro Gln Gly Thr Thr Glu  
 385 390

&lt;210&gt; 1095

&lt;211&gt; 1419

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1396)

&lt;223&gt; RXC02624

&lt;400&gt; 1095

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ggcagctcag caatcaaagt tgctgcgttt ccttccaacc gtg ctg att ccg cat 115

															Val	Leu	Ile	Pro	His	
															1				5	
ggc	gtg	gcg	gtg	ctt	ttg	gtt	att	att	ctc	gcc	gta	gcc	tcc	cta	atg	163				
Gly	Val	Ala	Val	Leu	Leu	Val	Ile	Ile	Leu	Ala	Val	Ala	Ser	Leu	Met					
				10					15					20						
ttc	acc	aat	tct	tca	atg	gtg	aat	ctt	tcg	gca	acg	att	gca	cag	ctg	211				
Phe	Thr	Asn	Ser	Ser	Met	Val	Asn	Leu	Ser	Ala	Thr	Ile	Ala	Gln	Leu					
				25					30					35						
tgg	ctt	tcc	cta	aat	ctc	ggt	gcg	gtg	gac	ggc	agt	ggg	gaa	gtg	atc	259				
Trp	Leu	Ser	Leu	Asn	Leu	Gly	Ala	Val	Asp	Gly	Ser	Gly	Glu	Val	Ile					
				40					45					50						
tca	gta	ctg	ccc	acg	ctt	ccc	ggc	ttt	ata	ttc	ctc	tgg	gcc	atc	gcc	307				
Ser	Val	Leu	Pro	Thr	Leu	Pro	Gly	Phe	Ile	Phe	Leu	Trp	Ala	Ile	Ala					
				55					60					65						
gcg	cgc	atc	cac	cgc	gca	gtc	aaa	gat	cgt	gtc	agc	atc	gcc	gac	tta	355				
Ala	Arg	Ile	His	Arg	Ala	Val	Lys	Asp	Arg	Val	Ser	Ile	Ala	Asp	Leu					
				70					75					80						
ggc	gtc	ctc	gca	gca	ctc	gtc	ctc	ggc	atc	ccg	ctt	gcg	ctc	acc	gcc	403				
Gly	Val	Leu	Ala	Ala	Leu	Val	Leu	Gly	Ile	Pro	Leu	Ala	Leu	Thr	Ala					
				90					95					100						
atc	gca	gcg	ttc	atg	ctt	ttc	gac	gcc	tcc	agc	gtc	ctc	aac	gtc	gag	451				
Ile	Ala	Ala	Phe	Met	Leu	Phe	Asp	Ala	Ser	Ser	Val	Leu	Asn	Val	Glu					
				105					110					115						
gtc	ccg	cca	atc	acg	cgc	ctc	cta	cgc	gtg	atg	ttg	ttc	cac	ctc	agc	499				
Val	Pro	Pro	Ile	Thr	Arg	Leu	Leu	Arg	Val	Met	Leu	Phe	His	Leu	Ser					
				120					125					130						
gcc	ctc	ttc	ctc	ggc	atg	ggg	cca	cgc	ctg	tgg	cag	gcg	ttg	gcg	cgc	547				
Ala	Leu	Phe	Leu	Gly	Met	Gly	Pro	Arg	Leu	Trp	Gln	Ala	Leu	Ala	Arg					
				135					140					145						
cgc	tac	ggt	gct	cca	gaa	tgg	ctt	atc	gac	gcc	atc	acc	caa	gct	ttc	595				
Arg	Tyr	Gly	Ala	Pro	Glu	Trp	Leu	Ile	Asp	Ala	Ile	Thr	Gln	Ala	Phe					
				150					155					160						
cgc	ttc	ctc	atc	gca	ttt	gga	aca	gtc	tcc	ttg	gtt	tcc	gtg	ctc	gtg	643				
Arg	Phe	Leu	Ile	Ala	Phe	Gly	Thr	Val	Ser	Leu	Val	Ser	Val	Leu	Val					
				170					175					180						
atg	acc	gcg	atc	aac	cac	agt	gca	ttc	acc	gcg	acc	atg	cag	ggt	tac	691				
Met	Thr	Ala	Ile	Asn	His	Ser	Ala	Phe	Thr	Ala	Thr	Met	Gln	Gly	Tyr					
				185					190					195						
gac	gac	tcc	gcc	tct	gtt	gtg	gcc	ttg	atc	gtc	ctg	agc	att	ctg	tat	739				
Asp	Asp	Ser	Ala	Ser	Val	Val	Ala	Leu	Ile	Val	Leu	Ser	Ile	Leu	Tyr					
				200					205					210						
ctg	ccc	aac	atg	atg	atc	ttt	gcg	atg	ggc	aat	ctg	atc	ggc	tca	ccc	787				
Leu	Pro	Asn	Met	Met	Ile	Phe	Ala	Met	Gly	Asn	Leu	Ile	Gly	Ser	Pro					
				215					220					225						
ctt	tac	ttc	ggt	gac	gcc	tcc	atc	agc	gtc	ttc	agc	gtg	cat	tcc	gtt	835				
Leu	Tyr	Phe	Gly	Asp	Ala	Ser	Ile	Ser	Val	Phe	Ser	Val	His	Ser	Val					

230	235	240	245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc				883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu	250	255	260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg				931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp	265	270	275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca				979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala	280	285	290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga				
1027				
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly	295	300	305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt				
1075				
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val	310	315	320	325
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga				
1123				
Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly	330	335	340	
atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg				
1171				
Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val	345	350	355	
gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag				
1219				
Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu	360	365	370	
cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg				
1267				
His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly	375	380	385	
gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct				
1315				
Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro	390	395	400	405
gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa				
1363				
Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu	410	415	420	
gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt				
1416				
Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg	425	430		

ctg  
1419

&lt;210&gt; 1096

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1096

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala  
 1 5 10 15

Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala  
 20 25 30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly  
 35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe  
 50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val  
 65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro  
 85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser  
 100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met  
 115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp  
 130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala  
 145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu  
 165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala  
 180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val  
 195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn  
 210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe  
 225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu  
 245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala  
 260 265 270

Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val  
 275 280 285

Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala  
 290 295 300  
 Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn  
 305 310 315 320  
 Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly  
 325 330 335  
 Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys  
 340 345 350  
 Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu  
 355 360 365  
 Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu  
 370 375 380  
 Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp  
 385 390 395 400  
 Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr  
 405 410 415  
 Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg  
 420 425 430

&lt;210&gt; 1097

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; RXC02665

&lt;400&gt; 1097

caaggcgacc caatggcggt taaagtaaca acccccattg atatgatgct ggcacaacgc 60  
 atcaccgacg aagccgaacc cacaatattt gaggtaccag gtg act aac cca atc 115  
 Val Thr Asn Pro Ile  
 1 5  
 atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga 163  
 Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly  
 10 15 20  
 aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211  
 Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys  
 25 30 35  
 gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259  
 Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala  
 40 45 50



ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg 307  
 Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val  
 55 60 65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355  
 Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu  
 70 75 80 85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403  
 Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala  
 90 95 100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa 451  
 Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu  
 105 110 115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct 499  
 Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser  
 120 125 130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547  
 Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg  
 135 140 145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600  
 Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala  
 150 155 160

ggc 603

&lt;210&gt; 1098

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1098

Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His  
 1 5 10 15

Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu  
 20 25 30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His  
 35 40 45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly  
 50 55 60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr  
 65 70 75 80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val  
 85 90 95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly  
 100 105 110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala  
 115 120 125

Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly  
 130 135 140  
 Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala  
 145 150 155 160

<210> 1099  
 <211> 1689  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1666)  
 <223> RXC02770

<400> 1099  
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 ttcacacatg ttgtttcgga agtcacgcag cgcggtaatc atg ttg gtt gca gcg 115  
 Met Leu Val Ala Ala  
 1 5  
 tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163  
 Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His  
 10 15 20  
 caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211  
 Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr  
 25 30 35  
 aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259  
 Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala  
 40 45 50  
 gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307  
 Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met  
 55 60 65  
 att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355  
 Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn  
 70 75 80 85  
 cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403  
 Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly  
 90 95 100  
 cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451  
 Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln  
 105 110 115  
 atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag 499  
 Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu  
 120 125 130  
 cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547  
 Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys

135	140	145	
gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg			595
Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu			
150	155	160	165
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag			643
Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu			
	170	175	180
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct			691
Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro			
	185	190	195
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag			739
Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu			
	200	205	210
ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg ggt gaa ttc			787
Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe			
	215	220	225
ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg			835
Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala			
230	235	240	245
gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc			883
Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala			
	250	255	260
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag			931
Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu			
	265	270	275
agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att			979
Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile			
	280	285	290
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc			
1027			
Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala			
	295	300	305
ggc gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt			
1075			
Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val			
310	315	320	325
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat			
1123			
Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp			
	330	335	340
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg			
1171			
Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val			
	345	350	355
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat			
1219			
His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn			

360 365 370  
 gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga  
 1267  
 Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly  
 375 380 385  
 ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt  
 1315  
 Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys  
 390 395 400 405  
 gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt  
 1363  
 Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser  
 410 415 420  
 ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag  
 1411  
 Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln  
 425 430 435  
 tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat  
 1459  
 Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His  
 440 445 450  
 cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg  
 1507  
 Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr  
 455 460 465  
 agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta  
 1555  
 Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu  
 470 475 480 485  
 gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt  
 1603  
 Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val  
 490 495 500  
 gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg  
 1651  
 Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp  
 505 510 515  
 tcc aga agt gag gaa taagtagtga gcgaacaagc tct  
 1689  
 Ser Arg Ser Glu Glu  
 520

&lt;210&gt; 1100

&lt;211&gt; 522

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1100

Met Leu Val Ala Ala Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro  
 1 5 10 15

Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser  
                   20                                  25                                  30  
 Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp  
                   35                                  40                                  45  
 Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly  
                   50                                  55                                  60  
 Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val  
                   65                                  70                                  75                                  80  
 Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala  
                                   85                                  90                                  95  
 Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser  
                   100                                  105                                  110  
 Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu  
                   115                                  120                                  125  
 Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala  
                   130                                  135                                  140  
 Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe  
                   145                                  150                                  155                                  160  
 Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly  
                                   165                                  170                                  175  
 Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu  
                   180                                  185                                  190  
 Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser  
                   195                                  200                                  205  
 Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp  
                   210                                  215                                  220  
 Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr  
                   225                                  230                                  235                                  240  
 Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly  
                                   245                                  250                                  255  
 Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His  
                   260                                  265                                  270  
 Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu  
                   275                                  280                                  285  
 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu  
                   290                                  295                                  300  
 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala  
                   305                                  310                                  315                                  320  
 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser  
                                   325                                  330                                  335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His  
 340 345 350  
 Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met  
 355 360 365  
 Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg  
 370 375 380  
 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala  
 385 390 395 400  
 Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser  
 405 410 415  
 Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu  
 420 425 430  
 Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg  
 435 440 445  
 Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr  
 450 455 460  
 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val  
 465 470 475 480  
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg  
 485 490 495  
 Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp  
 500 505 510  
 Asn Met Asp Arg Trp Ser Arg Ser Glu Glu  
 515 520

&lt;210&gt; 1101

&lt;211&gt; 408

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; RXC02238

&lt;400&gt; 1101

ggcgcttagc caaaacatag agcggtaggg tatgcttata cgattgagca acctttcccg 60

ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115  
 Val Thr Asn Val Ser  
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr  
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
           40                          45                          50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
           55                          60                          65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
           70                          75                          80                          85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                                   90                                  95

cac 408

<210> 1102

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1102

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp  
   1                          5                          10                          15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys  
           20                          25                          30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg  
           35                          40                          45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe  
           50                          55                          60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile  
           65                          70                          75                          80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                           85                          90                          95

<210> 1103

<211> 1298

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1275)

<223> RXC01946

<400> 1103

atc cgc aag tac tcc agg ctc gag gaa caa ttc cag tcg ctc ggc ggc 48  
 Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly  
   1                          5                          10                          15

tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96

Tyr	Glu	Ala	Asp	Ala	Glu	Ala	Ala	Gln	Ile	Cys	Asp	Asn	Leu	Gly	Leu	
			20					25					30			
gag	gca	cgc	atc	ctc	gac	cag	cag	ctt	aaa	acc	ctg	tcc	ggc	ggc	cag	144
Glu	Ala	Arg	Ile	Leu	Asp	Gln	Gln	Leu	Lys	Thr	Leu	Ser	Gly	Gly	Gln	
		35				40					45					
cgc	cgc	cgc	gtc	gag	ttg	gcg	cag	atc	ctc	ttc	gcc	gcc	acc	aac	ggc	192
Arg	Arg	Arg	Val	Glu	Leu	Ala	Gln	Ile	Leu	Phe	Ala	Ala	Thr	Asn	Gly	
	50					55				60						
tcc	ggc	aaa	tca	aaa	acc	aca	ttg	ctt	ctc	gac	gag	ccc	acc	aac	cac	240
Ser	Gly	Lys	Ser	Lys	Thr	Thr	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His	
65					70				75					80		
ttg	gac	gca	gac	tcg	atc	acc	tgg	ctc	cgt	gac	ttc	ctg	gcg	aag	cac	288
Leu	Asp	Ala	Asp	Ser	Ile	Thr	Trp	Leu	Arg	Asp	Phe	Leu	Ala	Lys	His	
				85				90						95		
gaa	ggt	gga	ctg	atc	atg	att	tcg	cac	gac	gtc	gaa	ctg	ctt	ggc	gcc	336
Glu	Gly	Gly	Leu	Ile	Met	Ile	Ser	His	Asp	Val	Glu	Leu	Leu	Gly	Ala	
			100					105					110			
gta	tgt	aac	aag	att	tgg	tac	ctc	gac	gca	gta	cgc	agc	gaa	gcc	gat	384
Val	Cys	Asn	Lys	Ile	Trp	Tyr	Leu	Asp	Ala	Val	Arg	Ser	Glu	Ala	Asp	
		115					120					125				
gtc	tac	aac	atg	ggc	ttt	agc	aaa	tac	gtc	gat	gca	cgt	gca	ctc	gat	432
Val	Tyr	Asn	Met	Gly	Phe	Ser	Lys	Tyr	Val	Asp	Ala	Arg	Ala	Leu	Asp	
	130					135				140						
gaa	gca	cgc	cga	cgc	cgt	gag	cgc	gca	aac	gcc	gaa	aag	aag	gcc	gga	480
Glu	Ala	Arg	Arg	Arg	Arg	Glu	Arg	Ala	Asn	Ala	Glu	Lys	Lys	Ala	Gly	
145					150				155					160		
gcc	ctc	aag	gac	cag	gct	gca	cgc	ctc	ggc	gcg	aaa	gca	acc	aag	gct	528
Ala	Leu	Lys	Asp	Gln	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Ala	Thr	Lys	Ala	
				165				170					175			
gcc	gca	gct	aag	cag	atg	atc	gcc	cgt	gcg	gaa	cga	atg	atc	gac	aac	576
Ala	Ala	Ala	Lys	Gln	Met	Ile	Ala	Arg	Ala	Glu	Arg	Met	Ile	Asp	Asn	
			180					185					190			
ctc	gac	gaa	atc	cgc	gta	gct	gac	cgc	gcc	gcc	aac	atc	gtt	ttc	cca	624
Leu	Asp	Glu	Ile	Arg	Val	Ala	Asp	Arg	Ala	Ala	Asn	Ile	Val	Phe	Pro	
		195				200						205				
gaa	cca	gca	ccc	tgt	gga	aaa	acc	cca	ctc	aac	gcc	aag	ggc	ctg	acc	672
Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr	
	210					215					220					
aag	atg	tac	ggc	tcc	ctc	gaa	gtc	ttc	gcc	ggc	gtc	gac	cta	gcc	atc	720
Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile	
225					230				235					240		
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggt	gca	ggt	aaa	768
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys	
				245				250						255		
acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggt	gtg	gaa	cgc	acc	gac	ggc	gaa	816
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu	



260	265	270	
ggc ggc atc gtc acc gga tac	ggc ctc aaa atc ggc tac	ttc gcc cag	864
Gly Gly Ile Val Thr Gly Tyr	Gly Leu Lys Ile Gly Tyr	Phe Ala Gln	
275	280	285	
gaa cac gac acc atc gac ccc gac	aaa tcc gtc tgg caa aac acc atc		912
Glu His Asp Thr Ile Asp Pro	Asp Lys Ser Val Trp Gln Asn Thr Ile		
290	295	300	
gaa gcc tgc gcc gac gcc gac	caa caa agc ctc cgc agc ctc ctc	gga	960
Glu Ala Cys Ala Asp Ala Asp	Gln Gln Ser Leu Arg Ser Leu Leu	Gly	
305	310	315	320
tcc ttc atg ttc tcc ggc gaa	caa ctc gac caa cca gca gga	aca ctc	
1008			
Ser Phe Met Phe Ser Gly	Glu Gln Leu Asp Gln Pro Ala Gly	Thr Leu	
325	330	335	
tcc ggc ggt gaa aaa acc cgc	ctc gca ctg gcc acc ctc gtg	tcc tcc	
1056			
Ser Gly Gly Glu Lys Thr Arg	Leu Ala Leu Ala Thr Leu Val	Ser Ser	
340	345	350	
cgc gca aac gtc ctg ctt ctc	gac gag ccc acc aac aac ctt	gac ccg	
1104			
Arg Ala Asn Val Leu Leu Leu	Asp Glu Pro Thr Asn Asn Leu	Asp Pro	
355	360	365	
atc tcc cgc gaa cag gtc ctc	gac gca ctg cgc acc tac acc	ggc gca	
1152			
Ile Ser Arg Glu Gln Val Leu	Asp Ala Leu Arg Thr Tyr Thr	Gly Ala	
370	375	380	
gtc gtc ctg gtt acc cac gac	ccg ggt gca gtc aag gcc ctt	gag cca	
1200			
Val Val Leu Val Thr His Asp	Pro Gly Ala Val Lys Ala Leu	Glu Pro	
385	390	395	400
gaa cgc gtc atc gtg ctt cct	gat ggc acc gag gat ctt tgg	aat gat	
1248			
Glu Arg Val Ile Val Leu Pro	Asp Gly Thr Glu Asp Leu Trp	Asn Asp	
405	410	415	
cag tac atg gaa atc gtg gaa	ttg gcg taggttctaa ggctgtttat		
1295			
Gln Tyr Met Glu Ile Val Glu	Leu Ala		
420	425		

gct  
1298

<210> 1104  
 <211> 425  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1104  
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Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu  
 20 25 30  
 Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln  
 35 40 45  
 Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly  
 50 55 60  
 Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His  
 65 70 75 80  
 Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His  
 85 90 95  
 Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala  
 100 105 110  
 Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp  
 115 120 125  
 Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp  
 130 135 140  
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly  
 145 150 155 160  
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala  
 165 170 175  
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn  
 180 185 190  
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro  
 195 200 205  
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr  
 210 215 220  
 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile  
 225 230 235 240  
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys  
 245 250 255  
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu  
 260 265 270  
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln  
 275 280 285  
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile  
 290 295 300  
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly  
 305 310 315 320  
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu  
 325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser  
340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro  
355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala  
370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro  
385 390 395 400

Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp  
405 410 415

Gln Tyr Met Glu Ile Val Glu Leu Ala  
420 425

<210> 1105

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXN03171

<400> 1105

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cggtcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115  
Met Asp Ile Thr Ile  
1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165

gac gca ttg gcg gaa tct  
 Asp Ala Leu Ala Glu Ser 613  
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<210> 1106  
 <211> 171  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1106  
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
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Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser  
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<210> 1107

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<211> 613
<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA02857
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Met Asp Ile Thr Ile																	
1 5																	
gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag																	163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu																	
10 15 20																	
cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc																	211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala																	
25 30 35																	
atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac																	259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp																	
40 45 50																	
acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca																	307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro																	
55 60 65																	
ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca																	355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro																	
70 75 80 85																	
gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc																	403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala																	
90 95 100																	
cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca																	451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro																	
105 110 115																	
cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc																	499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala																	
120 125 130																	
acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc																	547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly																	
135 140 145																	
gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg																	595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val																	
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gac gca ttg gcg gaa tct																	613
Asp Ala Leu Ala Glu Ser																	
170																	

<210> 1108  
 <211> 171  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1108

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Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
          35           40           45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
          50           55           60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
          65           70           75           80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
          85           90           95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
          100          105          110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
          115          120          125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
          130          135          140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
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Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> (101)..(424)  
 <223> RXN00450

<400> 1109

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
                               Val Gly Val Leu Pro
                               1           5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
          10           15           20

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gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211  
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val  
                   25                                  30                                  35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259  
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg  
                   40                                  45                                  50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307  
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg  
                   55                                  60                                  65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr  
                   70                                  75                                  80                                  85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403  
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val  
                                   90                                  95                                  100

ggt gct cga atc gga cgc atc 424  
 Gly Ala Arg Ile Gly Arg Ile  
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<210> 1110

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1110

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg  
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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
                   20                                  25                                  30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
                   35                                  40                                  45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
                   50                                  55                                  60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
                   65                                  70                                  75                                  80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
                                   85                                  90                                  95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile  
                   100                                  105

<210> 1111

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

**<400> 1111**

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gttttgataa tgatctgggt cgggtgggtgg gattcgacta	115
Val Gly Val Leu Pro	5
1	
gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg	163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu	20
10 15	
gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc	211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val	35
25 30	
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga	259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg	50
40 45	
gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga	307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg	65
55 60	
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc	355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr	85
70 75 80	
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg	403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val	100
90 95	
ggt gct cga atc gga	418
Gly Ala Arg Ile Gly	
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**<210> 1112**

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

**<400> 1112**

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Met	Arg	His	Ala	Leu	Asp	Ile	Ala	Arg	Gln	Thr	Pro	Glu	Gly	Asp	Val
			20					25					30		
Pro	Val	Gly	Ala	Val	Ile	Tyr	Ala	Pro	Thr	Gly	Glu	Ile	Leu	Ala	Thr
		35					40					45			
Ala	Thr	Asn	Arg	Arg	Glu	Ala	Asp	Arg	Asp	Pro	Thr	Ala	His	Ala	Glu
	50					55					60				
Ile	Ile	Ala	Leu	Arg	Arg	Ala	Ala	Arg	Arg	Phe	Ser	Asp	Gly	Trp	Arg
65					70					75					80
Leu	Ser	Asp	Cys	Thr	Ala	Val	Val	Thr	Leu	Glu	Pro	Cys	Ser	Met	Cys
				85					90					95	



Ala Gly Ala Leu Val Gly Ala Arg Ile Gly  
100 105

<210> 1113  
<211> 615  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(592)  
<223> RXA00465

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Met Thr Glu Asp Asp  
1 5  
tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163  
Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys  
10 15 20  
cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211  
Gln Gly Asn Ser Pro Tyr Gly Ser Leu Val Asp Pro Phe Gly Ala  
25 30 35  
gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259  
Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys  
40 45 50  
cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307  
His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala  
55 60 65  
tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355  
Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala  
70 75 80 85  
atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403  
Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys  
90 95 100  
gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451  
Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala  
105 110 115  
gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499  
Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn  
120 125 130  
ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547  
Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu  
135 140 145  
ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592  
Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu  
150 155 160

tagcgctggg catgtgactt taa

615

&lt;210&gt; 1114

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1114

Met Thr Glu Asp Asp Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala  
 1 5 10 15

Thr Gln Ala Leu Lys Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val  
 20 25 30

Asp Pro Phe Gly Ala Val Val Phe Glu Asp His Asn Arg Asp Ala Asp  
 35 40 45

Gly Asp Leu Thr Lys His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile  
 50 55 60

Glu Asn Tyr Ser Ala Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser  
 65 70 75 80

Thr Glu His Cys Ala Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu  
 85 90 95

Gly Lys Ile Tyr Cys Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr  
 100 105 110

Ala Lys Trp Gly Ala Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp  
 115 120 125

Lys Ile Ser Pro Asn Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu  
 130 135 140

Glu Val Leu Tyr Glu Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro  
 145 150 155 160

Asn Lys Ala Leu

&lt;210&gt; 1115

&lt;211&gt; 1083

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1060)

&lt;223&gt; RXA00717

&lt;400&gt; 1115

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 Val Thr Pro Pro Ala  
 1 5

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga	163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly	
10 15 20	
tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac	211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn	
25 30 35	
aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct	259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala	
40 45 50	
aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg	307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met	
55 60 65	
ggc ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg	355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val	
70 75 80 85	
ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att	403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile	
90 95 100	
gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc	451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly	
105 110 115	
gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc	499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg	
120 125 130	
atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt	547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg	
135 140 145	
ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt	595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly	
150 155 160 165	
gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc	643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val	
170 175 180	
ggc cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat	691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp	
185 190 195	
ggc gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag	739
Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys	
200 205 210	
act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc	787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser	
215 220 225	
gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac	835
Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp	
230 235 240 245	
ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc	883

Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile  
 250 255 260  
 gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931  
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu  
 265 270 275  
 ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979  
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val  
 280 285 290  
 cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct  
 1027  
 Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser  
 295 300 305  
 gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg  
 1080  
 Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 310 315 320  
 cct  
 1083  
 <210> 1116  
 <211> 320  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 1116  
 Val Thr Pro Pro Ala Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser  
 1 5 10 15  
 Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly  
 20 25 30  
 Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile  
 35 40 45  
 Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp  
 50 55 60  
 Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val  
 65 70 75 80  
 Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His  
 85 90 95  
 Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile  
 100 105 110  
 Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg  
 115 120 125  
 Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val  
 130 135 140  
 Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly  
 145 150 155 160

Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln  
 165 170 175  
 Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu  
 180 185 190  
 Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys  
 195 200 205  
 Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr  
 210 215 220  
 Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly  
 225 230 235 240  
 Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys  
 245 250 255  
 Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg  
 260 265 270  
 Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr  
 275 280 285  
 Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg  
 290 295 300  
 Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 305 310 315 320

<210> 1117  
 <211> 978  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(955)  
 <223> RXA01894

<400> 1117  
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 acccatgaat gaaccggagc aacatcaccg gtccatgagg atg ccc aaa ccc aaa 115  
 Met Pro Lys Pro Lys  
 1 5  
 aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163  
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly  
 10 15 20  
 ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211  
 Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp  
 25 30 35  
 tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259  
 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly

40	45	50	
agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile 55 60 65			307
atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met 70 75 80 85			355
ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe 90 95 100			403
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg 105 110 115			451
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly 120 125 130			499
agc ttc gct gcg atg ctg tgc ctg atg caa aac aat tcc atc ccg ggt Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly 135 140 145			547
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tgc gat gtg Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val 150 155 160 165			595
ggc ggg tat atc gcg ggt gtg ttc ttt gga tgc cac cca atg gcg ccg Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro 170 175 180			643
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val 185 190 195			691
tta gga tgc gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His 200 205 210			739
cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala 215 220 225			787
acg ttg ggt gac ttg gtt gag tgc cag ttc aaa cgc gat ttg ggc atc Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile 230 235 240 245			835
aag gat atg tgc aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg 250 255 260			883
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser 265 270 275			931
gtg atc agc agc tgc tat ccg tgc taaagcttgg gccagcttta agt Val Ile Ser Ser Ser Tyr Pro Ser 280 285			978

&lt;210&gt; 1118

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1118

Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile  
 1 5 10 15

Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu  
 20 25 30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala  
 35 40 45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro  
 50 55 60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp  
 65 70 75 80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu  
 85 90 95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala  
 100 105 110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp  
 115 120 125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn  
 130 135 140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val  
 145 150 155 160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser  
 165 170 175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe  
 180 185 190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His  
 195 200 205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala  
 210 215 220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys  
 225 230 235 240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly  
 245 250 255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr  
 260 265 270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser  
 275 280 285

<210> 1119  
 <211> 879  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(856)  
 <223> RXA02536

<400> 1119

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gcgtattgcc ttgcttcaga tctcgacgaa ttccgataag atg gac aac ttc gcc 115  
 Met Asp Asn Phe Ala  
 1 5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163  
 Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val  
 10 15 20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211  
 Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu  
 25 30 35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259  
 Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg  
 40 45 50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307  
 Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr  
 55 60 65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355  
 Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn  
 70 75 80 85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403  
 Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys  
 90 95 100

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451  
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys  
 105 110 115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499  
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly  
 120 125 130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547  
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu  
 135 140 145

gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595  
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp  
 150 155 160 165

ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643  
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala



170	175	180	
ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca			691
Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro			
185	190	195	
gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc			739
Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser			
200	205	210	
atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag			787
Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu			
215	220	225	
cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att			835
Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile			
230	235	240	245
cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act			879
Arg Glu Ala Leu Pro Val Leu			
250			
<210> 1120			
<211> 252			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1120			
Met Asp Asn Phe Ala Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu			
1	5	10	15
Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe			
20	25	30	
Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe			
35	40	45	
Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val			
50	55	60	
Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr			
65	70	75	80
Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His			
85	90	95	
Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu			
100	105	110	
Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp			
115	120	125	
Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu			
130	135	140	
Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro			
145	150	155	160
Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu			
165	170	175	

Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly  
 180 185 190

Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr  
 195 200 205

Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala  
 210 215 220

Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser  
 225 230 235 240

Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu  
 245 250

<210> 1121

<211> 1528

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1528)

<223> RXN01209

<400> 1121

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ctttatgcag tggatgcccc ggctgtggcc tcgttggttg atg tgc gag agg cct 115  
 Met Cys Glu Arg Pro  
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211  
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259  
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val  
 40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307  
 Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala  
 55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355  
 Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu  
 70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403  
 Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln  
 90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451  
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu  
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499  
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly  
 120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547  
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala  
 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595  
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu  
 150 155 160 165

atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643  
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly  
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691  
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp  
 185 190 195

ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct 739  
 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala  
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787  
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu  
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835  
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn  
 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883  
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr  
 250 255 260

ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931  
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly  
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123  
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355  
  
 agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370  
  
 ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385  
  
 gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405  
  
 cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420  
  
 ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435  
  
 gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459  
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450  
  
 tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465  
  
 gcc gcc ggc gaa agc gtg gaa  
 1528  
 Ala Ala Gly Glu Ser Val Glu  
 470 475

&lt;210&gt; 1122

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1122

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
 1 5 10 15  
  
 Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
 20 25 30  
  
 Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
 35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365  
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn

370	375	380
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met		
385	390	395 400
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr		
	405	410 415
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn		
	420	425 430
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg		
	435	440 445
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser		
	450	455 460
Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu		
465	470	475

&lt;210&gt; 1123

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; FRXA01209

&lt;400&gt; 1123

cagattgcag cacagaaggc atcggcgcca ggcagctttg cggtggcggtt tattgatgcg 60

ctttatgacg tggatgcccc ggctgtggcc tcgttggttg atg tgc gag agg cct	115
Met Cys Glu Arg Pro	
1 5	

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt	163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val	
10 15 20	

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att	211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile	
25 30 35	

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
40 45 50	

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
55 60 65	

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451  
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu  
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499  
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly  
 120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547  
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala  
 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595  
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu  
 150 155 160 165

atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643  
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly  
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691  
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp  
 185 190 195

ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct 739  
 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala  
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787  
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu  
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835  
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn  
 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883  
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr  
 250 255 260

ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931  
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly  
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465

gcc gcc ggc gaa agc gtg gaa  
 1528

Ala Ala Gly Glu Ser Val Glu  
 470 475

<210> 1124

<211> 476

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1124

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
 1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
 20 25 30



Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
 35 40 45  
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

355	360	365
Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn		
370	375	380
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met		
385	390	395
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr		
	405	410
		415
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn		
	420	425
		430
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg		
	435	440
		445
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser		
	450	455
		460
Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu		
465	470	475

&lt;210&gt; 1125

&lt;211&gt; 795

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(772)

&lt;223&gt; RXN01617

&lt;400&gt; 1125

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tgtttatggc attgggtcca tcacatgctt gggtggcctt	ttg atc cta aag aca	115
	Leu Ile Leu Lys Thr	
	1 5	

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat	163
Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn	
	10 15 20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc	211
Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile	
	25 30 35

ggc atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg	259
Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu	
	40 45 50

gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc	307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys	
	55 60 65

aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc	355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg	
	70 75 80 85

gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403  
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu  
                     90                    95                    100

gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451  
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu  
                     105                    110                    115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499  
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val  
                     120                    125                    130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547  
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu  
                     135                    140                    145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595  
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp  
                     150                    155                    160                    165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643  
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala  
                     170                    175                    180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691  
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys  
                     185                    190                    195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739  
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro  
                     200                    205                    210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc 792  
 Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
                     215                    220

cct 795

<210> 1126

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala  
     1                    5                    10                    15

Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu  
                     20                    25                    30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
                     35                    40                    45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
                     50                    55                    60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
                     65                    70                    75                    80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr

85							90					95				
Pro	Asn	Asn	Phe	Glu	Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu	
			100				105						110			
Thr	Ile	Asp	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly	
			115				120						125			
Pro	Gln	Tyr	Val	Val	Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn	
			130				135						140			
Ala	Val	Asp	Val	Leu	Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu	
145				150						155			160			
Pro	Lys	Ile	Gly	Asp	Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala	
			165						170			175				
Ala	Val	Ile	Thr	Ala	Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala	
			180						185			190				
Val	Thr	Thr	Ala	Lys	Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val	
			195						200			205				
Ala	Ser	Asn	Ala	Pro	Phe	Thr	Ser	Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys	
			210						215			220				

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<210> 1127
<211> 638
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (1)..(615)  
<223> FRXA01617
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<400> 1127																
gct	aat	cag	att	gag	gcc	gcc	acc	gca	gcg	cac	gat	ctt	gat	gtg	gtg	48
Ala	Asn	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu	Asp	Val	Val	
1				5					10					15		
aag	atc	ggt	atg	ttg	ggt	act	cct	gca	acg	atc	gat	act	gtg	gca	acc	96
Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr	
			20					25					30			
gct	ttg	gag	gaa	aac	agc	ttc	aag	cac	gtt	gtc	cta	gac	ccg	gta	ctg	144
Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu	
		35					40					45				
atc	tgc	aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc	192
Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala	
	50					55					60					
ctt	cgc	gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	gtt	act	cca	aac	aac	240
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn	
65					70					75				80		

ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac 288  
 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp  
                     85                    90                    95

gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac 336  
 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr  
                     100                    105                    110

gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac 384  
 Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
                     115                    120                    125

gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc 432  
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile  
                     130                    135                    140

ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc 480  
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
                     145                    150                    155                    160

acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc 528  
 Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
                     165                    170                    175

gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576  
 Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
                     180                    185                    190

gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt 625  
 Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
                     195                    200                    205

aaacaagctc cct 638

&lt;210&gt; 1128

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1128

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val  
   1                    5                    10                    15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
                     20                    25                    30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu  
                     35                    40                    45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala  
                     50                    55                    60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn  
                     65                    70                    75                    80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp  
                     85                    90                    95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr  
                     100                    105                    110

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile  
130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
195 200 205

<210> 1129

<211> 792

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(769)

<223> RXC01600

<400> 1129

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tttggagctg cgtgtccacc cttagatcta caatgtgatc atg gtt tgc aag atg 115  
Met Val Ser Lys Met  
1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163  
His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu  
10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211  
Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro  
25 30 35

ggg ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259  
Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val  
40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307  
Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr  
55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355  
Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu  
70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403  
Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met  
90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451  
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu  
 105 110 115

att acc tgc cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499  
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala  
 120 125 130

cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547  
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu  
 135 140 145

gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595  
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met  
 150 155 160 165

gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643  
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met  
 170 175 180

gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691  
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr  
 185 190 195

gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739  
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala  
 200 205 210

cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789  
 His Gly Ile Val Pro Asp Met Lys Lys Leu  
 215 220

aaa 792

&lt;210&gt; 1130

&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1130

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr  
 1 5 10 15

Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp  
 20 25 30

Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu  
 35 40 45

His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala  
 50 55 60

Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu  
 65 70 75 80

Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala  
 85 90 95

Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser  
 100 105 110

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val  
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val  
 130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His  
 145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala  
 165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser  
 180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala  
 195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu  
 210 215 220

<210> 1131  
 <211> 726  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(703)  
 <223> RXC01622

<400> 1131  
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gccatcgag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115  
 Met Ser Asp Phe Tyr  
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163  
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly  
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211  
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg  
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259  
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val  
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307  
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu  
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355  
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro  
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403



Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val  
                                     90                                    95                                    100  
 gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451  
 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val  
                                     105                                    110                                    115  
 cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499  
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu  
                                     120                                    125                                    130  
 ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547  
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu  
                                     135                                    140                                    145  
 aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595  
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro  
                                     150                                    155                                    160                                    165  
 tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643  
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met  
                                     170                                    175                                    180  
 cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691  
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp  
                                     185                                    190                                    195  
 cct tca gat aat tagatgagtt ccgaaaattt aaa 726  
 Pro Ser Asp Asn  
                                     200  
  
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 <211> 201  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
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     1                                    5                                    10                                    15  
 Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser  
                                     20                                    25                                    30  
 Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala  
                                     35                                    40                                    45  
 Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala  
                                     50                                    55                                    60  
 Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu  
                                     65                                    70                                    75                                    80  
 Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val  
                                     85                                    90                                    95  
 Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu  
                                     100                                    105                                    110  
 Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val  
                                     115                                    120                                    125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp  
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val  
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile  
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Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser  
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Thr Phe Pro Ser Asp Pro Ser Asp Asn  
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<210> 1133

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 1133

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115  
 Val Ser Lys Ile Ser  
 1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163  
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val  
 10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211  
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg  
 25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259  
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro  
 40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307  
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala  
 55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355  
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly  
 70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403  
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg  
 90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451  
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile  
 105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499  
 Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr  
 120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547  
 Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu  
 135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595  
 Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu  
 150 155 160 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt 643  
 Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe  
 170 175 180

gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat 691  
 Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn  
 185 190 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt 739  
 Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly  
 200 205 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat 787  
 Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp  
 215 220 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg 835  
 Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu  
 230 235 240 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg 883  
 Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val  
 250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931  
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala  
 265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979  
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp  
 280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg  
 1027  
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu  
 295 300 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg  
 1075  
 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val  
 310 315 320 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg  
 1123  
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala  
 330 335 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac  
 1171  
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn  
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg  
 1219  
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala  
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt  
 1267  
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser  
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga  
 1315  
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg  
 1363  
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu  
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act  
 1411  
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc  
 1459  
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag  
 1507  
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
 455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca  
 1555  
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
 470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg  
 1603  
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
 490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat  
 1651  
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
 505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac  
 1699  
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
 520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat  
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg  
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc

1827

Val Ala Tyr

<210> 1134

<211> 568

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1134

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400  
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro

530

535

540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr  
 545 550 555 560

Arg Ala Ala Pro Val Val Ala Tyr  
 565

&lt;210&gt; 1135

&lt;211&gt; 555

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(532)

&lt;223&gt; RXC01709

&lt;400&gt; 1135

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gaaattaggt gtcgatgcag caatacggaa ctttgccaat gtg ttt gaa caa gct 115  
 Val Phe Glu Gln Ala  
 1 5

ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg 163  
 Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Ala Gly  
 10 15 20

ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc 211  
 Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser  
 25 30 35

ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca 259  
 Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala  
 40 45 50

cag gca gat tta gtc atc act gga gaa gga gcg att gat gca cag acc 307  
 Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr  
 55 60 65

ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa 355  
 Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys  
 70 75 80 85

gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca 403  
 Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala  
 90 95 100

atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa 451  
 Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu  
 105 110 115

tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt 499  
 Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly  
 120 125 130

atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552  
 Ile Gly Phe Asn Ile Ala Lys His His Leu Ser  
 135 140

gat

555

&lt;210&gt; 1136

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1136

Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly  
 1 5 10 15

Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser  
 20 25 30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly  
 35 40 45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg  
 50 55 60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys  
 65 70 75 80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser  
 85 90 95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser  
 100 105 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu  
 115 120 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser  
 130 135 140

&lt;210&gt; 1137

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(898)

&lt;223&gt; RXC02207

&lt;400&gt; 1137

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ggccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115  
 Met Arg Arg Arg Ser  
 1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163  
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala  
 10 15 20



ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg	211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met	
25 30 35	
ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc	259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly	
40 45 50	
caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt	307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly	
55 60 65	
gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc	355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val	
70 75 80 85	
tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa	403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln	
90 95 100	
tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc	451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala	
105 110 115	
gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg	499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu	
120 125 130	
cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat	547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp	
135 140 145	
cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc	595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg	
150 155 160 165	
gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag	643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln	
170 175 180	
ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc	691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr	
185 190 195	
tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt	739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg	
200 205 210	
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt	787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly	
215 220 225	
ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att	835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile	
230 235 240 245	
gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc	883
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro	
250 255 260	

cac cga cga gga acc  
His Arg Arg Gly Thr  
265

898

&lt;210&gt; 1138

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1138

Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu  
1 5 10 15

Leu Ala Ser Thr Ala Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr  
20 25 30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala  
35 40 45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met  
50 55 60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu  
65 70 75 80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu  
85 90 95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe  
100 105 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro  
115 120 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala  
130 135 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu  
145 150 155 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala  
165 170 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp  
180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp  
195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val  
210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu  
225 230 235 240

Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu  
245 250 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr  
260 265

<210> 1139  
 <211> 891  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(868)  
 <223> RXA00347

<400> 1139

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                                   Met Thr Leu Thr Ile
                                   1 5

gag gaa atc gcc aag acc aaa aag ctt ttg gtt gtg tcc gat ttt gat 163
Glu Glu Ile Ala Lys Thr Lys Lys Leu Leu Val Val Ser Asp Phe Asp
                                   10 15 20

gga acc atc gca gga ttt agc aag gac gct tac aac gtt cct atc aac 211
Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr Asn Val Pro Ile Asn
                                   25 30 35

cag aaa tcc ctc aag gcg gta aaa gac ctc tcc caa caa gca gac act 259
Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser Gln Gln Ala Asp Thr
                                   40 45 50

gat gtt gtc att ttg tgc gga cgt cac ctg gag gga ttg aag acg gtt 307
Asp Val Val Ile Leu Ser Gly Arg His Leu Glu Gly Leu Lys Thr Val
                                   55 60 65

ctt gat ctt ggt cag tac gac atc acc atg gtg ggt tca cac ggt tct 355
Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val Gly Ser His Gly Ser
                                   70 75 80 85

gag gat tcc tcc cgc ccg cgt acc ctc act cct gaa gag gta gct cgc 403
Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro Glu Glu Val Ala Arg
                                   90 95 100

ctc gcc aag att gaa gca gat ctg gaa aag atc gtc gac ggc atc gaa 451
Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile Val Asp Gly Ile Glu
                                   105 110 115

ggc gca ttc gtg gag atc aag cct ttc cac cgc gtg ctg cac ttc atc 499
Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg Val Leu His Phe Ile
                                   120 125 130

cgt gtt tcc gac aag gac aaa gtc caa gga atc ctc gcc caa gca gca 547
Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile Leu Ala Gln Ala Ala
                                   135 140 145

cac gta gac tct tcc ggc ctg aag gtt act aac ggc aag agc atc atc 595
His Val Asp Ser Ser Gly Leu Lys Val Thr Asn Gly Lys Ser Ile Ile
                                   150 155 160 165

gaa tac tcc atc agc tcc acc acc aag ggc acc tgg ctg aag gaa tac 643
Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr Trp Leu Lys Glu Tyr
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170										175										180										
gtt gac cgc acc gag ccc act ggt gtg att ttc ctc ggc gat gac acc	691																													
Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe Leu Gly Asp Asp Thr																														
185	190	195																												
acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta	739																													
Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu																														
200	205	210																												
acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac	787																													
Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp																														
215	220	225																												
gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc	835																													
Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg																														
230	235	240	245																											
atg cag tat gcg gaa agc gtg cga ttg ggg att taagagagcc taaacgcacg	888																													
Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile																														
250	255																													
aaa	891																													
<210> 1140																														
<211> 256																														
<212> PRT																														
<213> Corynebacterium glutamicum																														
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Met Thr Leu Thr Ile Glu Glu Ile Ala Lys Thr Lys Lys Leu Leu Val																														
1	5	10	15																											
Val Ser Asp Phe Asp Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr																														
20	25	30																												
Asn Val Pro Ile Asn Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser																														
35	40	45																												
Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu																														
50	55	60																												
Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val																														
65	70	75	80																											
Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro																														
85	90	95																												
Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile																														
100	105	110																												
Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg																														
115	120	125																												
Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile																														
130	135	140																												
Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn																														
145	150	155	160																											

Gly	Lys	Ser	Ile	Ile	Glu	Tyr	Ser	Ile	Ser	Ser	Thr	Thr	Lys	Gly	Thr	
				165					170					175		
Trp	Leu	Lys	Glu	Tyr	Val	Asp	Arg	Thr	Glu	Pro	Thr	Gly	Val	Ile	Phe	
				180					185					190		
Leu	Gly	Asp	Asp	Thr	Thr	Asp	Glu	His	Gly	Phe	Lys	Ala	Leu	Glu	Asn	
				195					200					205		
Asp	Asp	Arg	Ala	Leu	Thr	Val	Lys	Val	Gly	Glu	Gly	Asp	Thr	Ala	Ala	
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Lys	Thr	Arg	Val	Asp	Asp	Val	Asp	Asn	Val	Gly	Ile	Phe	Leu	Glu	Lys	
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					Met	Ala	Arg	Pro	Ile	5						
					1											
tcc	gca	acg	tac	agg	ctt	caa	atg	cga	gga	cct	caa	gca	gat	agc	gcc	163
Ser	Ala	Thr	Tyr	Arg	Leu	Gln	Met	Arg	Gly	Pro	Gln	Ala	Asp	Ser	Ala	
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ggg	cgt	tca	ttt	ggt	ttt	gcg	cag	gcc	aaa	gcc	cag	ctt	ccc	tat	ctg	211
Gly	Arg	Ser	Phe	Gly	Phe	Ala	Gln	Ala	Lys	Ala	Gln	Leu	Pro	Tyr	Leu	
			25					30					35			
aag	aag	cta	ggc	atc	agc	cac	ctg	tac	ctc	tcc	cct	att	ttt	acg	gcc	259
Lys	Lys	Leu	Gly	Ile	Ser	His	Leu	Tyr	Leu	Ser	Pro	Ile	Phe	Thr	Ala	
		40					45					50				
atg	cca	gat	tcc	aat	cat	ggc	tac	gat	gtc	att	gat	ccc	acc	acc	atc	307
Met	Pro	Asp	Ser	Asn	His	Gly	Tyr	Asp	Val	Ile	Asp	Pro	Thr	Thr	Ile	
	55					60					65					
aat	gaa	gag	ctc	ggt	ggc	atg	gag	ggt	ctt	cga	gat	ctt	gcc	gca	gct	355
Asn	Glu	Glu	Leu	Gly	Gly	Met	Glu	Gly	Leu	Arg	Asp	Leu	Ala	Ala	Ala	
	70				75					80					85	
aca	cac	gag	ttg	ggc	atg	ggc	atc	atc	att	gat	att	gtt	ccc	aac	cat	403
Thr	His	Glu	Leu	Gly	Met	Gly	Ile	Ile	Ile	Asp	Ile	Val	Pro	Asn	His	

	90	95	100	
tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta				451
Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu				
	105	110	115	
aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg				499
Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp				
	120	125	130	
cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt				547
His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly				
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gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag				595
Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu				
	150	155	160	165
aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc				643
Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr				
	170	175	180	
gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg				691
Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu				
	185	190	195	
cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg				739
Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val				
	200	205	210	
aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat				787
Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His				
	215	220	225	
act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc				835
Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly				
	230	235	240	245
gtg cgc gtc gat cac ccc gac ggg ctt tcc gat cct ttt gga tat ctg				883
Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu				
	250	255	260	
cac aga ctc cgc gac ctc att gga cct gac cgc tgg ctg atc atc gaa				931
His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu				
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aag atc ttg agc gtt gat gaa cca ctc gat ccc cgc ctg gcc gtt gat				979
Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp				
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ggc acc act ggc tac gac gcc ctc cgt gaa ctc gac ggc gtg ttt atc				
1027				
Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu Asp Gly Val Phe Ile				
	295	300	305	
tcc cga gaa tct gag gac aaa ttc tcc atg ctg gcg ctg acc cac agt				
1075				
Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu Ala Leu Thr His Ser				
	310	315	320	325

gga tcc acc tgg gat gaa cgc gcc ctc aaa tcc acg gag gaa agc ctc  
1123

Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu  
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aaa cga gtc gtc gcc caa caa gaa ctc gca gcc gaa atc tta agg ctc  
1171

Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu  
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gcc cgc gcc atg cgc cgc gat aac ttc tcc acc gca ggc acc aac gtc  
1219

Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val  
360 365 370

acc gaa gac aaa ctt agc gaa acc atc atc gaa tta gtc gcc gcc atg  
1267

Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met  
375 380 385

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1315

Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr  
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gtc atc gcg gag atg tcc aaa cgc ttc ccc tcc cgg cgt gac gca ctc  
1363

Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu  
410 415 420

gac ctc atc gcg gcc gcc cta ctt ggc aat ggc gag gcc aaa atc cgc  
1411

Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg  
425 430 435

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1459

Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr  
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Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly  
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1555

Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln  
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1603

Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr  
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1651

His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu  
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tct gaa gtc ccc gat atg tac tcc gag ctg gtc aat cgt gtt ttc gcg  
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Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp  
730 735 740

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Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile  
745 750 755

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760 765 770

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775 780 785

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Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg  
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Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp  
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Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp

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 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu  
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 Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met  
 485 490 495  
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala  
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 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile  
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 675 680 685  
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 690 695 700  
 Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His  
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 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile  
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 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr  
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Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr  
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Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
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 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala  
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 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile  
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 70 75 80 85

aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403  
 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His  
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tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta 451  
 Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu  
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 120 125 130

cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt 547  
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 135 140 145

gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag 595  
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 150 155 160 165

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 185 190 195

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act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc 835  
 Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly  
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 265 270 275

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 1027  
 Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu Asp Gly Val Phe Ile  
 295 300 305

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 375 380 385

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 1411  
 Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg  
 425 430 435

ttc gct caa gtc tgc ggc gcc gtc atg gct aaa ggt gtg gaa gac acc  
 1459  
 Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr  
 440 445 450

acc ttc tac cgc gca tct agg ctc gtt gca ttg caa gaa gtc ggt ggc  
 1507  
 Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly  
 455 460 465

gcg ccg ggg aga ttc ggc gtc tcc gct gca gaa ttc cac ttg ctg cag  
 1555  
 Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln  
 470 475 480 485

gaa gaa cgc agc ctg ctg tgg cca cgc acc atg acc acc ttg tcc acg  
 1603  
 Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr  
 490 495 500

cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg  
 1651  
 His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu  
 505 510 515

tct gaa gtc ccc gat atg tac tcc gag ctg gtc aat cgt gtt ttc gcg  
 1699  
 Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala  
 520 525 530

gtg ctc ccc gcg cca gac ggc gca acg ggc agt ttc ctc cta caa aac  
 1747  
 Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn  
 535 540 545

ctg ctg ggc gta tgg ccc gcc gac ggc gtg atc acc gat gcg ctg cgc  
1795  
Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile Thr Asp Ala Leu Arg  
550 555 560 565

gat cga ttc agg gaa tac gcc cta aaa gct atc cgc gaa gca tcc aca  
1843  
Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr  
570 575 580

aaa acc acg tgg gtg gac ccc aac gag tcc ttc gag gct gcg gtc tgc  
1891  
Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys  
585 590 595

gat tgg gtg gaa gcg ctt ttc gac gga ccc tcc acc tca cta atc acc  
1939  
Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser Thr Ser Leu Ile Thr  
600 605 610

gaa ttt gtc tcc cac atc aac cgt ggc tct gtg caa atc tcc tta ggc  
1987  
Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly  
615 620 625

agg aaa ctg ctg caa atg gtg ggc gct gga atc ccc gac act tac caa  
2035  
Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln  
630 635 640 645

gga act gag ttt tta gaa gac tcc ctg gta gat ccc gat aac cga cgc  
2083  
Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg  
650 655 660

ttt gtt gat tac acc gcc aga gaa caa gtc ctg gag cgc ctg caa acc  
2131  
Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu Glu Arg Leu Gln Thr  
665 670 675

tgg gat tgg acg cag gtt aat tcg gta gaa gac ttg gtg gat aac gcc  
2179  
Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala  
680 685 690

gac atc gcc aaa atg gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct  
2227  
Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala  
695 700 705

gaa ttt cgt gca agc ttt gtt ggt gga gat cat cag gca gta ttt ggc  
2275  
Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly  
710 715 720 725

gaa ggt cgc gca gaa tcc cac atc atg ggc atc gcc cgc ggt aca gac  
2323  
Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp  
730 735 740

cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc  
2371

Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile  
745 750 755

ttg gaa gac cgt ggc gga tgg tat gac acc acc gtc acg ctt cct ggt  
2419

Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly  
760 765 770

gga caa tgg gaa gac agg ctc acc ggg caa cgc ttc agt ggt gtt gtc  
2467

Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val  
775 780 785

cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta  
2515

Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu  
790 795 800 805

gta ccc gat agt gag ttt tgatccctgc acaggaaagt tag  
2556

Val Pro Asp Ser Glu Phe  
810

<210> 1144

<211> 811

<212> PRT

<213> Corynebacterium glutamicum

<400> 1144

Met Ala Arg Pro Ile Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro  
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Gln Ala Asp Ser Ala Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala  
20 25 30

Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser  
35 40 45

Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile  
50 55 60

Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg  
65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp  
85 90 95

Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp  
100 105 110

Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr  
115 120 125

Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly  
130 135 140

Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala  
145 150 155 160



Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro  
 165 170 175  
 Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg  
 180 185 190  
 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg  
 195 200 205  
 Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro  
 210 215 220  
 Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu  
 225 230 235 240  
 Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp  
 245 250 255  
 Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg  
 260 265 270  
 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro  
 275 280 285  
 Arg Leu Ala Val Asp Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu  
 290 295 300  
 Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu  
 305 310 315 320  
 Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser  
 325 330 335  
 Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala  
 340 345 350  
 Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr  
 355 360 365  
 Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu  
 370 375 380  
 Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser  
 385 390 395 400  
 Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser  
 405 410 415  
 Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly  
 420 425 430  
 Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys  
 435 440 445  
 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu  
 450 455 460  
 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu  
 465 470 475 480

Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met  
 485 490 495  
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala  
 500 505 510  
 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val  
 515 520 525  
 Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser  
 530 535 540  
 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile  
 545 550 555 560  
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile  
 565 570 575  
 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe  
 580 585 590  
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser  
 595 600 605  
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val  
 610 615 620  
 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile  
 625 630 635 640  
 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp  
 645 650 655  
 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu  
 660 665 670  
 Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp  
 675 680 685  
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser  
 690 695 700  
 Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His  
 705 710 715 720  
 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile  
 725 730 735  
 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr  
 740 745 750  
 Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr  
 755 760 765  
 Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
 770 775 780  
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 785 790 795 800  
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810

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<220>  
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<222> (101)..(1930)  
<223> RXA02645
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170	175 180
cgc aat tgg ggc tac gac ggg gtg ctg tgg cac gcc gtc cat gca ggc	691
Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His Ala Val His Ala Gly	
185	190 195
tac ggc ggt ccg gcg ggc ttg aaa aag ctt atc gac gcc tcc cac cag	739
Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile Asp Ala Ser His Gln	
200	205 210
gcc ggc atc gcc gtc tac tta gac gtc gtg tac aac cac ttc ggc ccc	787
Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr Asn His Phe Gly Pro	
215	220 225
gac ggc aac tac aac ggg caa ttt ggc ccc tac acc tct ggc ggc agc	835
Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr Thr Ser Gly Gly Ser	
230	235 240 245
acc ggc tgg ggc gac gtg gtc aac atc aac ggc cat gat tca gat gaa	883
Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly His Asp Ser Asp Glu	
250	255 260
gtc cgc aat tat att ctc gac gcc gca cgc cag tgg ttc gaa gat ttt	931
Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln Trp Phe Glu Asp Phe	
265	270 275
cac gtt gat ggg ctc cgc ctc gat gcg gtg cat tct ctc gat gat cgc	979
His Val Asp Gly Leu Arg Leu Asp Ala Val His Ser Leu Asp Asp Arg	
280	285 290
ggc gcc tat tcc cta ctt gcg cag ctg acc atg gtg gcc gag gat gtc	
1027	
Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met Val Ala Glu Asp Val	
295	300 305
tcc gca caa aca ggc atc cca cgc tca ttg att gca gaa tct gaa ctc	
1075	
Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile Ala Glu Ser Glu Leu	
310	315 320 325
aat gac ccc aag ttc gtt acc tcc cgc gag gcc ggc ggt ttt ggc ctg	
1123	
Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala Gly Gly Phe Gly Leu	
330	335 340
gat gca cag tgg gtt gac gat atc cac cac gcc ctc cat gcc ctc gtt	
1171	
Asp Ala Gln Trp Val Asp Asp Ile His His Ala Leu His Ala Leu Val	
345	350 355
tct ggc gaa cgc aat ggt tat tac agc gat ttc gga tct gtc gac aca	
1219	
Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe Gly Ser Val Asp Thr	
360	365 370
tta gcc aaa acc ctg cgt gaa gta ttt gaa cac acc gga aac tac tcc	
1267	
Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His Thr Gly Asn Tyr Ser	
375	380 385

gag ctg att tac agc ttc act tcc ccc acc gtc acc gac acc tcc aca  
1891

Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val Thr Asp Thr Ser Thr  
585 590 595

acc ctt cag ccg tgg ggc ttt gcg atc ctg acc cga aac tagaaaaagg  
1940

Thr Leu Gln Pro Trp Gly Phe Ala Ile Leu Thr Arg Asn  
600 605 610

ccacctcgat tga  
1953

<210> 1146

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 1146

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Cys His Ser Ile Ser His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr  
20 25 30

Ser Leu Val Ala Met Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro  
35 40 45

Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met  
50 55 60

His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala  
65 70 75 80

Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys  
85 90 95

Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly  
100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp  
115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly  
130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro  
145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln  
165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His  
180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile  
195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr  
210 215 220

acg tac cgc gga cgc aac cac ggc cgc cct gtg cac ccc gat atc acc  
 1315  
 Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val His Pro Asp Ile Thr  
 390 395 400 405  
 cct gcc tcg cgc ttt gtc acc tac acc acc acc cat gat cag acc ggc  
 1363  
 Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr His Asp Gln Thr Gly  
 410 415 420  
 aac cgc gca atc ggc gac cgt cct tcc acg act ctc acc ccg gaa cag  
 1411  
 Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr Leu Thr Pro Glu Gln  
 425 430 435  
 cag gtg ttg aag gca gcc att atc tac agc tcg ccg tat acc ccg atg  
 1459  
 Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser Pro Tyr Thr Pro Met  
 440 445 450  
 ttg ttt atg ggt gaa gaa ttc gga gcc acc acc cca ttc gcc ttc ttt  
 1507  
 Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr Pro Phe Ala Phe Phe  
 455 460 465  
 tgc tcc cac acc gac ccc gag ctc aac cgg cta acc tcc gag ggc cgc  
 1555  
 Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu Thr Ser Glu Gly Arg  
 470 475 480 485  
 aaa cgg gaa ttc gca cgc ctt ggc tgg aac gcc gac gac atc ccc tcc  
 1603  
 Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser  
 490 495 500  
 ccc gag ctg gaa tcc acc ttc acc tcc tcc aaa ctc gat tgg gag ttc  
 1651  
 Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe  
 505 510 515  
 act gcg gag cag cgc cgc atc aac gac gct tac aag cag ctg ttg cac  
 1699  
 Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr Lys Gln Leu Leu His  
 520 525 530  
 ctg cgg cac acc ttg ggc ttc tcc caa cca aac ttg ctc aca ctc gag  
 1747  
 Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn Leu Leu Thr Leu Glu  
 535 540 545  
 gtt gag cac ggc gag aac tgg cta tcg atg gcc aat ggt cgc ggc cga  
 1795  
 Val Glu His Gly Glu Asn Trp Leu Ser Met Ala Asn Gly Arg Gly Arg  
 550 555 560 565  
 att ctg gcg aat ttc tcc gac gac acc atc acc gtc ccg ctt ggc ggc  
 1843  
 Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr Val Pro Leu Gly Gly  
 570 575 580

Asn His Phe Gly Pro Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr  
 225 230 235 240  
 Thr Ser Gly Gly Ser Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly  
 245 250 255  
 His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln  
 260 265 270  
 Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His  
 275 280 285  
 Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met  
 290 295 300  
 Val Ala Glu Asp Val Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile  
 305 310 315 320  
 Ala Glu Ser Glu Leu Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala  
 325 330 335  
 Gly Gly Phe Gly Leu Asp Ala Gln Trp Val Asp Asp Ile His His Ala  
 340 345 350  
 Leu His Ala Leu Val Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe  
 355 360 365  
 Gly Ser Val Asp Thr Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His  
 370 375 380  
 Thr Gly Asn Tyr Ser Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val  
 385 390 395 400  
 His Pro Asp Ile Thr Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr  
 405 410 415  
 His Asp Gln Thr Gly Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr  
 420 425 430  
 Leu Thr Pro Glu Gln Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser  
 435 440 445  
 Pro Tyr Thr Pro Met Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr  
 450 455 460  
 Pro Phe Ala Phe Phe Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu  
 465 470 475 480  
 Thr Ser Glu Gly Arg Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala  
 485 490 495  
 Asp Asp Ile Pro Ser Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys  
 500 505 510  
 Leu Asp Trp Glu Phe Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr  
 515 520 525  
 Lys Gln Leu Leu His Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn  
 530 535 540

Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala  
 545 550 555 560

Asn Gly Arg Gly Arg Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr  
 565 570 575

Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val  
 580 585 590

Thr Asp Thr Ser Thr Thr Leu Gln Pro Trp Gly Phe Ala Ile Leu Thr  
 595 600 605

Arg Asn  
 610

<210> 1147

<211> 832

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(832)

<223> RXN02355

<400> 1147

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tagattgata agcatctgtt gttaagaaag gtgacttcct atg tcc tcg att tcc 115  
 Met Ser Ser Ile Ser  
 1 5

cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163  
 Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile  
 10 15 20

gca ctg gcc ggt tgt agt tca gac tca agc tcc gac tcc aca gat tcc 211  
 Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser  
 25 30 35

acc gct agc gaa ggc gca gac agc cgc ggc ccc atc acc ttt gcg atg 259  
 Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met  
 40 45 50

ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307  
 Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn  
 55 60 65

gaa gcc cac ccc gat gag cag gta acg ctc aac gaa ctc gcc ggt gaa 355  
 Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn Glu Leu Ala Gly Glu  
 70 75 80 85

gcc gac gcg cag cgc gaa acc ctc gtg caa tcc ctg cag gcc ggc aac 403  
 Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser Leu Gln Ala Gly Asn  
 90 95 100

tct gac tac gac gtc atg gcg ctc gac gtc atc tgg acc gca gac ttc 451  
 Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe  
 105 110 115



gcg gca aac caa tgg ctc gca cca ctt gaa ggc gac ctc gag gta gac 499  
 Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly Asp Leu Glu Val Asp  
           120                                  125                                  130

acc tcc gga ctg ctg caa tcc acc gtg gat tcc gca acc tac aac ggc 547  
 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly  
           135                                  140                                  145

acc ctc tac gca ctg cca cag aac acc aac ggc cag cta ctg ttc cgc 595  
 Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly Gln Leu Leu Phe Arg  
           150                                  155                                  160                                  165

aac acc gaa atc atc cca gaa gca cca gca aac tgg gct gac ctc gtg 643  
 Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn Trp Ala Asp Leu Val  
                                   170                                  175                                  180

gaa tcc tgc acg ctt gct gaa gaa gca ggc gtt gat tgc ctg acc act 691  
 Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val Asp Cys Leu Thr Thr  
                                   185                                  190                                  195

cag ctc aag cag tac gaa ggc ctt tca gtg aac acc atc ggc ttc atc 739  
 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile  
                                   200                                  205                                  210

gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787  
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg  
           215                                  220                                  225

aga cag cac gac ggc aag gca ggc ctt caa gcg ctt gtc gac ggc 832  
 Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala Leu Val Asp Gly  
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&lt;210&gt; 1148

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1148

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           20                                  25                                  30

Asp Ser Thr Asp Ser Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro  
           35                                  40                                  45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile  
           50                                  55                                  60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn  
           65                                  70                                  75                                  80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser  
                                   85                                  90                                  95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile  
           100                                  105                                  110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115	120	125
Asp Leu Glu Val Asp Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser 130 135 140		
Ala Thr Tyr Asn Gly Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly 145 150 155 160		
Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn 165 170 175		
Trp Ala Asp Leu Val Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val 180 185 190		
Asp Cys Leu Thr Thr Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn 195 200 205		
Thr Ile Gly Phe Ile Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp 210 215 220		
Gly Lys Arg His Arg Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala 225 230 235 240		
Leu Val Asp Gly		

&lt;210&gt; 1149

&lt;211&gt; 609

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(586)

&lt;223&gt; RXN02909

&lt;400&gt; 1149

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atagtttcct ggattgtttg gcacagtcgg gagaaaactc	atg aac cgc gca cga	115
	Met Asn Arg Ala Arg	
	1 5	

atc gcg acc ata ggc gtt ctt ccg ctt gct tta ctg ctg gcg tcc tgt	163
Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Leu Ala Ser Cys	
10 15 20	

ggt tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat	211
Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn	
25 30 35	

att tac acc gat cca gat gag tcg aat tcg atc agt aat ctt gtc att	259
Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile	
40 45 50	

tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act	307
Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Leu Ser Gly Phe Thr	
55 60 65	

ggc tgt gtg cct ttt acg ggg cgt gcg gaa ttc ttc caa aat ggt gag	355
---	-----

Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu  
 70 75 80 85  
 caa agc tct gtt ctg gat gcc gat tat gtg acc ttg tct tcc ctg gat 403  
 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp  
 90 95 100  
 ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451  
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His  
 105 110 115  
 aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499  
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr  
 120 125 130  
 tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547  
 Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val Asp Glu Leu Asp Arg  
 135 140 145  
 cca gca atc cgc ttg gtg tcc tgg atc gcg ccg aca tct taagggtgcca 596  
 Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro Thr Ser  
 150 155 160  
 gggctttaa gtg 609

&lt;210&gt; 1150

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1150

Met Asn Arg Ala Arg Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu  
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 Leu Leu Ala Ser Cys Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr  
 20 25 30  
 Trp Leu Val Thr Asn Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile  
 35 40 45  
 Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser  
 50 55 60  
 Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe  
 65 70 75 80  
 Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr  
 85 90 95  
 Leu Ser Ser Leu Asp Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln  
 100 105 110  
 Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe  
 115 120 125  
 Glu Ile Ser Arg Thr Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val  
 130 135 140  
 Asp Glu Leu Asp Arg Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro  
 145 150 155 160

Thr Ser

&lt;210&gt; 1151

&lt;211&gt; 1590

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1567)

&lt;223&gt; RXS00349

&lt;400&gt; 1151

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                                         Met Leu Ser Phe Ala
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acc ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct 163
Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro
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ccg cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg 211
Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val
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gcc ggt gtg atg aat ttg gct gcg aga att gcc gat att ttg ctt tct 259
Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser
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tca ggt acg tca aat agt gac acc aag gta caa gtt cga gca gtg acc 307
Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr
          55          60          65

tct gcg tac ggt ttg tac tac acg cac gtg gat atc acg ttg aat acg 355
Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp Ile Thr Leu Asn Thr
          70          75          80          85

atc acc atc ttc acc aac atc ggt gtg gag agg aag atg ccg gtc aac 403
Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn
          90          95          100

gtg ttt cat gtt gta ggc aag ttg gac acc aac ttc tcc aaa ctg tct 451
Val Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser
          105          110          115

gag gtt gac cgt ttg atc cgt tcc att cag gct ggt gcg acc ccg cct 499
Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala Gly Ala Thr Pro Pro
          120          125          130

gag gtt gcc gag aaa atc ctg gac gag ttg gag caa tcc cct gcg tct 547
Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser
          135          140          145

tat ggt ttc cct gtt gcg ttg ctt ggc tgg gca atg atg ggt ggt gct 595
Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala Met Met Gly Gly Ala
          150          155          160          165

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gtt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt 643  
 Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe  
 170 175 180

att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag 691  
 Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys  
 185 190 195

ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg 739  
 Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr  
 200 205 210

ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag 787  
 Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu  
 215 220 225

atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca 835  
 Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala  
 230 235 240 245

ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg 883  
 Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro  
 250 255 260

gtg aca gca agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc 931  
 Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly  
 265 270 275

att gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat 979  
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gtc atg ttg cct gcc atg gag tcc gct gca gca cct aat tat tcg tct  
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aca ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca  
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 345 350 355

ccc gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt  
 1219  
 Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly  
 360 365 370

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 Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile

375                                      380                                      385  
 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg  
 1315  
 Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met  
 390                                      395                                      400                                      405  
 tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att ggc  
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 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala  
 410                                      415                                      420  
 gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt  
 1411  
 Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly  
 425                                      430                                      435  
 gag tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac  
 1459  
 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr  
 440                                      445                                      450  
 cgt gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag  
 1507  
 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu  
 455                                      460                                      465  
 cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc  
 1555  
 Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe  
 470                                      475                                      480                                      485  
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 Gly Asn Lys Arg

&lt;210&gt; 1152

&lt;211&gt; 489

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1152

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 Ala Lys Ala Ala Pro Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr  
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 Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly  
 35                                      40                                      45  
 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln  
 50                                      55                                      60  
 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp  
 65                                      70                                      75                                      80  
 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg  
 85                                      90                                      95

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn  
 100 105 110  
 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala  
 115 120 125  
 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu  
 130 135 140  
 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala  
 145 150 155 160  
 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val  
 165 170 175  
 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser  
 180 185 190  
 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly  
 195 200 205  
 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu  
 210 215 220  
 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile  
 225 230 235 240  
 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly  
 245 250 255  
 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu  
 260 265 270  
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu  
 275 280 285  
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala  
 290 295 300  
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr  
 305 310 315 320  
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile  
 325 330 335  
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 340 345 350  
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala  
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 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
 370 375 380  
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala  
 385 390 395 400  
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
 405 410 415

Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala  
 420 425 430

Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro  
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Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe  
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Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys  
 465 470 475 480

Thr Asn Gln Arg Phe Gly Asn Lys Arg  
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&lt;210&gt; 1153

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(417)

&lt;223&gt; RXS03183

&lt;400&gt; 1153

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aaa gac ggc gtc ggc gta tcc acc ctt ggt ggc tac aac aac ggc atc 96  
 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile  
 20 25 30

aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc 144  
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
 35 40 45

atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca 192  
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
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cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240  
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80

cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288  
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95

cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336  
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110

gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384  
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
 115 120 125

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 <212> PRT  
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 35 40 45  
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
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 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80  
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95  
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110  
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
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 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser  
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<210> 1155  
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 <212> DNA  
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<220>  
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 <222> (101)..(1189)  
 <223> RXC00874

<400> 1155  
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 Met Ser Ile Gly Gln  
 1 5  
 cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163  
 His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp  
 10 15 20  
 aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211

Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly Glu Asn Thr Leu Ala	
25 30 35	
gta gtg cgc atc aac aat gcg ctg tat cag ttg ttg gtc aat gat gat	259
Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp	
40 45 50	
ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc	307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe	
55 60 65	
gga gca tgg act ggc agc tct gct ttt ccc att ggc cct ttc act cca	355
Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro	
70 75 80 85	
ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa	403
Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys	
90 95 100	
gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat	451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp	
105 110 115	
gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc	499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile	
120 125 130	
ctg ggt ttt tcc tcc gct gag atc tcc ggg gct aac tac acc ctg gtc	547
Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val	
135 140 145	
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg	595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu	
150 155 160 165	
act act acc tct ggc agc ttt gca gag gat gca gaa aag atc ggc gaa	643
Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu	
170 175 180	
gcc acc cgc aat gtt cac act gct ctt gca tgc gcc ttc cct act cgg	691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg	
185 190 195	
gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat	739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn	
200 205 210	
gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc	787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala	
215 220 225	
atc gac ctc tac caa tgc ttg gaa ggc gaa gcc cac atc caa cgc atc	835
Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile	
230 235 240 245	
cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac	883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr	
250 255 260	
atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga	931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg	

265 270 275  
 cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc 979  
 Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser  
 280 285 290  
 atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac  
 1027  
 Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn  
 295 300 305  
 gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa  
 1075  
 Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln  
 310 315 320 325  
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 Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala  
 330 335 340  
 tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg  
 1171  
 Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1156  
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 Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu  
 35 40 45  
 Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu  
 50 55 60  
 Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile  
 65 70 75 80  
 Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile  
 85 90 95  
 Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser  
 100 105 110  
 Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro  
 115 120 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala  
 130 135 140  
 Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly  
 145 150 155 160  
 Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala  
 165 170 175  
 Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser  
 180 185 190  
 Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu  
 195 200 205  
 Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg  
 210 215 220  
 Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala  
 225 230 235 240  
 His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys  
 245 250 255  
 Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg  
 260 265 270  
 Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala  
 275 280 285  
 Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His  
 290 295 300  
 Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly  
 305 310 315 320  
 Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala  
 325 330 335  
 Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys  
 340 345 350  
 Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp  
 355 360

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4 January 2001 (04.01.2001)

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| 60/141,031   | 25 June 1999 (25.06.1999) | US | 199 33 004.2 | 14 July 1999 (14.07.1999)     | DE |
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| 199 31 415.2 | 8 July 1999 (08.07.1999)  | DE | 60/148,613   | 12 August 1999 (12.08.1999)   | US |
| 199 31 418.7 | 8 July 1999 (08.07.1999)  | DE | 199 40 764.9 | 27 August 1999 (27.08.1999)   | DE |
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| 199 31 424.1 | 8 July 1999 (08.07.1999)  | DE | 199 40 832.7 | 27 August 1999 (27.08.1999)   | DE |
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| 199 32 228.7 | 9 July 1999 (09.07.1999)  | DE |              |                               |    |
| 199 32 229.5 | 9 July 1999 (09.07.1999)  | DE |              |                               |    |
| 199 32 230.9 | 9 July 1999 (09.07.1999)  | DE |              |                               |    |
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| 199 32 926.5 | 14 July 1999 (14.07.1999) | DE |              |                               |    |
| 199 32 928.1 | 14 July 1999 (14.07.1999) | DE |              |                               |    |
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- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,

[Continued on next page]

(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING METABOLIC PATHWAY PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated MP nucleic acid molecules, which encode novel MP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MP proteins, mutated MP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MP genes in this organism.

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**(88) Date of publication of the international search report:**  
29 March 2001

— *With international search report.*

- Before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments.

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00923

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/31 C12N15/61 C12N1/21 C12N9/90 C07K14/34  
 C12P13/08 C12Q1/68  
 //(C12N15/61,C12R1:15)

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12P C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EP0-Internal, EMBL, BIOSIS

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>KEILHAUER C ET AL: "ISOLEUCINE SYNTHESIS IN CORYNEBACTERIUM GLUTAMICUM: MOLECULAR ANALYSIS OF THE ILVB-ILVN-ILVC OPERON" JOURNAL OF BACTERIOLOGY,US,WASHINGTON, DC, vol. 175, no. 17, 1 September 1993 (1993-09-01), pages 5595-5603, XP000611312 ISSN: 0021-9193 the whole document</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p>	<p>1-3, 8-19, 22-34</p>

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- "Z" document member of the same patent family

Date of the actual completion of the international search

31 October 2000

Date of mailing of the international search report

24. 01. 01

Name and mailing address of the ISA

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Galli, I

## INTERNATIONAL SEARCH REPORT

International Application No

PC., IB 00/00923

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL SEQUENCES [Online]  Accession No. 033231,  15 December 1998 (1998-12-15)  COLE S.T.: "Diaminopimelate epimerase  (DAPf) of Mycobacterium tuberculosis."  XP002151647  52% identity at amino acid level with Seq.  ID 2.  -&amp; COLE S.T. ET AL.: "Deciphering the  biology of Mycobacterium tuberculosis from  the complete genome sequence."  NATURE,  vol. 393, 1998, pages 537-544, XP002151645</p> <p>---</p>	6-17,37, 38
A	<p>BATHE B. ET AL.: "A physical and genetic  map of the Corynebacterium glutamicum  ATCC13032 chromosome."  MOL. GEN. GENET.,  vol. 252, 1996, pages 255-265, XP002151646  the whole document, in particular table 3.</p> <p>---</p>	1-38
A	<p>EP 0 435 132 A (KERNFORSCHUNGSANLAGE  JUELICH) 3 July 1991 (1991-07-03)  the whole document</p> <p>---</p>	1-38
A	<p>EIKMANN B J ET AL: "MOLECULAR ASPECTS OF  LYSINE, THREONINE, AND ISOLEUCINE  BIOSYNTHESIS IN CORYNEBACTERIUM  GLUTAMICUM"  ANTONIE VAN LEEUWENHOEK, DORDRECHT, NL,  vol. 64, no. 2, 1993, pages 145-163,  XP000918559  figure 1</p> <p>-----</p>	1-38



# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/IB 00/00923

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1-38 Partially.

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-38, partly

An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein or a portion thereof, said nucleic acid being characterized by sequence ID 1. An isolated nucleic acid comprising a nucleotide sequence at least 50% homologous to seq. 1. Corresponding polypeptides (Seq. ID 2). Corresponding vectors, recombinant host cells, production methods. Use in diagnosis of *C. diptheriae*.

### Information on patent family members

PC., iB 00/00923

Form PCT/ISA/210 (patent family annex) (July 1992)